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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
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PCT-US93-08528-45
US-08-858-876A-4
US-09-477-880-4
US-09-477-675A-10
US-09-077-675A-13
US-09-077-675A-3
US-09-077-675A-5
US-09-077-675A-3
US-09-077-675A-3
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US-09-261-599B-3
US-09-261-599B-3
US-09-456-455A-3
US-09-472-880-2
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US-09-4171-13-426-2
US-09-4171-3-426-2
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SWIYQC SWIYQC LQHQAN LQHQAN LQHQAN LQHQAN LQHQAN LQHQAN LQHQAN LQHQAN LQHQAN LQHQAN LQHQAN	Sequence 2, Application US/09545 Patent No. 6461836 GEMERAL INFORMATION: APPLICANT: AMES, ROBERT APPLICANT: ELSHOURBAGY, NABIL APPLICANT: SARAD, HENRY APPLICANT: SARAD, HENRY APPLICANT: VAWTER, LISA TITLE OF INVENTION: MOLECULAR TITLE OF INVENTION: (AXOR34) A FILE REFERENCE: GP70657-1 CURRENT APPLICATION NUMBER: US/ CURRENT FILING DATE: 2000-04-1 PRIOR APPLICATION NUMBER: US/ CURRENT FILING DATE: 1999-11-05 NUMBER OF SEQ ID NOS: 5 NUMBER OF SEQ ID NOS: 5 SOFTMARE: FASTSEQ FOR WINDOWS SEQ ID NO 2 LENGTH: 415 TYPE: PRT ORGANISM: HOMO SAPIENS SOFTMAC: 1999-18; Best Local Similarity 99.18; Best Local Similarity 99.68; Matches 239; Conservative 1	119.666 119.6666 119.6666
KLEDPFQ	JOHN US/0 JOHN JOHN JOHN JOHN JOHN JOHN JOHN JOHN	369 369 369 369 356 356 391 391 398 398 398 398 398
EYLAFLCGPRRSHFE	944 944 CLONING OF A 7TM ND SCREENING METH 09/545,944 09/435,384 Version 3.0 Version 3.0 Version 3.0 Score 1252; DB 4 Pred. No. 3e-107; Mismatches	4 US-08-387-707-9 4 US-08-405-271A-9 5 US-09-170-331-5 6 US-09-170-601B-9 6 US-08-430-286A-5 7 US-08-430-286A-5 7 US-08-454-549-3 7 US-08-454-549-3 7 US-08-454-552-3 7 US-08-108-252-3 7 US-08-11-245-5 7 US-08-1
LPVSVVYVPIEVVGVIGN 60	RECEPTOR ODS THEREOF Length 415; indels 0; Gaps	Sequence 9, Appl. Sequence 9, Appl. Sequence 5, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 5, Appl. Sequence 3, Appl. Sequence 3, Appl. Sequence 5, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 3, Appl.
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RESULT 2 US-08-118-270-45 ; Sequence 45, Application US/08118270

419 Seventh Street, N.W., Suite 300

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PCT-US93-08528-45
; Sequence 45, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                 NUMBER OF SEQUENCES: 3
                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10 - SEP - 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
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TELEPHONE: 202-737-3528
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
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REGISTRATION NUMBER: 34
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                                                           New York University

VENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                   RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.1%; Score 304; DB 1; Length 353; 33.3%; Pred. No. 1.9e-20; ative 49; Mismatches 73; Indels
                                   348
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RESULT 4
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                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Daniel (
APPLICANT: Pascale
APPLICANT: Pascual
APPLICANT: Vita NA:
                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                               Sequence 4, Application US/08858876A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                    TITLE OF INVENTION: Type 2 Neurotensin Receptor TITLE OF INVENTION: (hNT-R2)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 415 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 10-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        118
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                                                                                                                                                                                                                                                                                                                                                                                                                       159
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                           CITY: Washington STATE: D.C.
                COUNTRY:
                                                           STREET:
                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NFIWHHPWAFGDAGCRGYYF---LRDACTYATALNVASLSVERYLAICHPFKAKTLMSRS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 202 - 3528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Townsend, Kevin
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 VTAIYLALFVVGTVGNSVTAFTLARKKSLQSLQSTVHYHLSSLALSDLLILLW----VELY 60
                                                                                                                                                                                                                                                                                                                            FMSFLFPMLVISILNTVIANKLTV 199
                                                                                                                                                                                                                                                                                                                                                                                   RTKKFISAIWLASALLAIPMLFTLGLQNR--SGDGTHPGGLVCTPIVDTATVKVVIQVNT 175
                                                                                                                                                                                                                                                                                                                                                                                                                  RALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTS 218
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                                                           400 Seventh Street
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Pascual FERRARA
                                                                                                                                                      Vita NATALIO
                USA
                                                                                                                                                                                                   Daniel CAPUT
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                                                                          Jacobson, Price,
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Pred. No. 1.9e-20;
Pred. No. 1.9e-20;
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                                                                          Holman &
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Query Match
Best Local Similarity
Whiches 72; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09472880
Patent No. 6274333
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 WRNYPFLFGPVGC---YFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRA 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/
FILING DATE: 17-MAR-1997
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                              (hNT-R2)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Type 2 Neurotensin Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Daniel CAPUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRLLSLVWVASLGLALPMAVIMGQKHEVESADGEPEPASRVCTVLVSRATLQVFIQVNVL 212
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               APPLICATION NUMBER: US/09/472,880 FILING DATE: 28-Dec-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                        CITY: Washington STATE: D.C.
                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                         ADDRESSEE: Jacobson, Price STREET: 400 Seventh Street
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Pascual FERRARA
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Pred. No. 3e-18;
                                                                                                                                                                                                                                                                            Price, Holman & Stern,
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GENERAL INFORMATION:
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                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      ZIP: 07065-0900
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16
                                                 ATTORNEY/AGENT INFORMATION:
NAME: COCUZZO, Anna L.
REGISTRATION NUMBER: 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
TELECOMMUNICATION INFORMATION: TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                             APPLICATION NUMBER: US/
FILING DATE: 3-JUN-1998
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STATE:
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                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Merck & Co.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 SVVYVPIFVVGVIGNVLVCLVILQHQAMKT-PTNYYLFSLAVSDLLVLLLGMPLEVYE-M 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/FR 9723204
FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INCORMATION:
NAME: Player, William E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
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                                                                                                                                                                                                                                                                                                                                              USA
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Pred. No. 3e-18;
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Length 361; Indels

26;

Gaps

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US-09-077-675A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09077675A Patent No. 6242199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Pai, L
                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Howard, Andrew D.
APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16
CORRESSONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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CITY: R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 GIVWGFSVLFSLPNTSIHGIKFHYFPNGS------LVPGSATCTVIKPMWIYNF 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 ----SSIFFFLPVFCLTVLYSLIGRKL 239
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                                                                                                          TELEFAX: 732-594-4720
                                                                                                                                                                                                      NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,452
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 3-JUN
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Merck & Co., Inc.
P.O. Box 2000, 126 E. Lincoln Ave
361 amino acids
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Pred. No. 4.6e-18;
17; Mismatches 69;
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; Sequence 13, Application US/09077675A
; Patent No. 6242199
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APPLICANT: Pai, Lec
APPLICANT: Feighner
APPLICANT: Howard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                              INFORMATION FOR SEQ ID NO:
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STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: I
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: COCUZZO, Anna L.
REGISTRATION NUMBER: 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
CORRES
                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 -----SSIFFFLPVFCLTVLYSLIGRKL 234
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                TOPOLOGY:
                                    STRANDEDNESS:
                                                                                      LENGTH:
                                                                                                                                                                                                    TELEFAX: 732-594-4720
                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
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                                                                : 366 amino acids amino acid
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EDNESS: single
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                linear
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Wind
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/
                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 353 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Cocuzzo, Anna L.
                                                                    MOLECULE TYPE:
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APPLICATION NUMBER:
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 QYRPWNFGDLLCKLFQFVSESCTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVI 164
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                                                                                                                                                                                   TELEPHONE: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: F.U. CITY: Rahway
                                                                                                STRANDEDNESS:
                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                      NAME: COCUZZO, Anna L. REGISTRATION NUMBER: 42. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 VSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMW 104
                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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: Pong, Sheng-Shung
: Van Der Ploeg, Leonardus H.T.
: NVENTION: RECEPTOR ASSAY
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P.O. Box 2000, 126 E. Lincoln Ave.
                                                                                                                                 353 amino acids
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Howard, Andrew D.
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FastSEQ for Windows Version 2.0
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31.7%; Pred. No. 6e-18;
21.7%;
31.7%;
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Score 274; DB 4; Pred. No. 1.1e-17;
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               Length
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GENERAL INFORMATION:
                                              Matches
                                                            Query Match
Best Local S
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                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
1-077-675x-17
                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus H.T.
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Cocuzzo, Anna L.
                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 GIVWGFSVLFSLPNTSIHGIKFHYFPNGS------LVPGSATCTVIKPMWIYNF 212
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TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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                                                                                                                                                                                                                                                                                                  NAME: COCUZZO, Anna L
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                            TELEFAX: 732-594-4720
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Feighner, Scott C
Howard, Andrew D.
                                              Conservative
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                                                           21.7%;
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                                             Score 274; DB 4;
Pred. No. 1.1e-17;
7; Mismatches 69
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; STRANDEDNESS:
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US-09-077-675A-5
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                                                                                                                                                                                                                                                                                                   NAME: COCUZZO, Anna L. REGISTRATION NUMBER: 42,452 REFERENCE/DOCKET NUMBER: 19: TELECOMMUNICATION INFORMATION: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Howard, Andrew D.
APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus H.T.
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: US/
FILING DATE: 3-JUN-1998
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
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STREET: Rahway
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                                                           45 VSVVYVPIEVVGVIGNVLVCLVILQHQAMKTPTNYYLESLAVSDLLVLLLGMPLEVYEMW 104
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                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
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ZIP: 07065-0900
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VTATCVALFVVGIAGNLLTMLVVSRFREMRTTTNLYLSSMAFSELLIFLC-MPLELFRLW 104
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                                                                                                                                                                                                                    amino acid
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                                                                                                       Conservative
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                                                                                                                                                                           protein
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                                                                                                                21.6%; Score 273; DB 4; 31.7%; Pred. No. 1.1e-17;
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                                                                                                    47;
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                                                                                                    Mismatches
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Query Match
Best Local Similarity
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US-07-629-104I-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (203)268-1951 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 3.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gershengorn, Marvin C
APPLICANT: Straub, Richard E
TITLE OF INVENTION: PITUITARY TR
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                                                       157
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                   229
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                                                                                         175
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                                                                                                                             97
                                                                                                                                                                                            42 GNIMVVLVVMRTKHMRTPTNCYLVSLAVADLMVLVAAGLPNITDSIYGSW-----VYGYV
                                                                                                                                                                                                               59 GNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLL-LGMPL---EVYEMWRNYPFLFGPV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 ----SSVFFFLPVFCLTVLYSLIGRKL 239
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                                                                                                                                                                                                                                                                                                            15 LEDPFQKHLNSTE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 26 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 19901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Yanwan _
AMBRESSEE: Yanwan _
AMBRET: 25 Skytop Drive
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ISVLYYLMA 237
                                                                                                                                          GCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLF 174
                                                                                 SLPNTSIHGIKFHYFPNGSLVPGSATC----TVIKPMWIYNFIIQVTSFLFYLLPMTV 228
                                                                                                                                                                                                                                                                      MENDTVSEMNQTELQPQAAVALEYQVVTILLVVIICG-----
                                                 CMLWFFLLDLNISTYKNAVVV----SCGYKISRNYYSPIYLMDFGV-----FYVVPMIL
                                                                                                                       GCLCITYLQYLGINASSCSITAFTIERYIAICHPIKAQFLCTFSRAKKIIIFVWAFTSIY 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVIWAVAFCSAGPIFVLVGVE---HDNGTDPRDTNECRATEFAVRSGLLTVM--VWV---
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                                                                                                                                                                                                                                                                                                                                                48;
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                                                                                                                                                                                                                                                                                                                                             Score 265; DB 1; Length 393; Pred. No. 8.1e-17; Mismatches 69; Indels
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                                                                                        SEQ ID NO 3
LENGTH: 259
TYPE: PRT
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NUMBER OF SEQ ID NOS:
SOFTWARE: PATENTIN VE
EQ ID NO 3
LENGTH: 259
TYPE: PRT
ORGANISM: Unknown
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Best Local Similarity
Matches 67; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09456455A Patent No. 6448005
                                                                                                                                                                                                                                              APPLICANT: Glucksmann, Maria A.
APPLICANT: Tsai, Fong-Ying
TITLE OF INVENTION: 14273 Receptor, A No. (
FILE REFERENCE: MNI-204CP3
CURRENT APPLICATION NUMBER: US/09/456,455A
CURRENT FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: 09/107,761
PRIOR FILING DATE: 1998-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 14273 Receptor, A No. 6395877el G-Protein Coupled Receptor
EILE REFERENCE: 5800-44B, 035800/177086
CURRENT APPLICATION NUMBER: US/09/261,599B
CURRENT FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 09/107,761
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/223,538 PRIOR FILING DATE: 1998-12-30
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PRIOR FILING DATE: 1998-12-30
                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: OTHER INFORMATION:
OTHER INFORMATION: Description of Unknown Organism: Seven OTHER INFORMATION: Transmembrane Segment Rhodopsin Superfamily
                                            FEATURE:
                                                                   ORGANISM: Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 VLFSLPNTSIHGIKFHYFPNGSLVPGSATCTVIKP-----MWIYNFIIQVTSFLFYL 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SALCKLYTALDVVNMYASILLLTAISIDRYLAIVHPLRYRRRTSPRRAKVVILLVWVLA 115
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Transmembrane Segment Rhodopsin
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Pred. No. 8.7e-17
8; Mismatches 6
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Superfamily
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; MOLECULE TYPE: US-08-288-663A-1
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Best Local S
Matches 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 198309/1993
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: 286986/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 325215/1993
ETLING DATE: 22-DEC-1993
ETLING DATE: 22-DEC-1993
                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 44
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                           FILING DATE: 22-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION LONGER: US/08/288,663A FILING DATE: 09-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN TRH RECEPTOR, ITS PRODUCTION TITLE OF INVENTION: AND USE
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STREET: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 SALCKLVTALDVVNMYASILLLTAISIDRYLAIVHPLRYRRRRTSPRRAKVVILLVWVLA 115
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                                    TOPOLOGY:
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                                                                                                                                                                                                                       REGISTRATION NUMBER:
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                                                                       LENGTH:
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HOSOYA, Masaki
                                                                                                                                                 617-523-6440
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                                                                         amino acids
                 protein
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earch completed: January 17, 2003, 05:08:09 Cob time : 28 secs

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Title:
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TITLE OF INVENTION: No. 96436703el Nucleic F.
TITLE REFERENCE: 790C1P2A
CURRENT APPLICATION NUMBER: US/09/668,680
CURRENT FILING DATE: 2000-09-22
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                                           Conservative
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                                                      38.7%;
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                                       Score 282.4; DB 4; Pred. No. 9.9e-54; 0; Mismatches 211;
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                                        Indels
                                                                 Length
                                        0;
                                        Gaps
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RESULT 3
US-09-077-675A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,675A
FILING DATE: 3-JUN-1998
CLASSIFICATION:
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pai, Lee-Yuh
APPLICANT: Feighner, Scott C.
APPLICANT: Howard, Andrew D.
APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Lec
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                             STREET: P.O. CITY: Rahway
                                                                                                                                                                                                        ZIP: 07065-0900
                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                           ADDRESSEE: Merck & Co., Inc. STREET: P.O. Box 2000, 126 E. Lincoln
APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGACCACCGCGCTGCTCTTCTTCTGCCTGCCCATGGCCATCATGAGCGTGCTCTACCTG 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCACCGTCAGCGTGGAGCGCTACGTGGCCATCCTACACCCGTTCCGCGCCCAAACTGCAG 462
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                                                                   Sequence 9, Application US/09077675A Patent No. 6242199
GENERAL INFORMATION:
APPLICANT: Pai, Lee-Yuh
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lest Local :
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SEQUENCE CHARACTERISTICS:
LENGTH: 1088 base pairs
                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: COCUZZO, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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      APPLICANT:
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STRANDEDNESS: single
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Feighner, Scott C.
Howard, Andrew D.
Pong, Sheng-Shung
Van Der Ploeg, Leonardus
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Best Local S
Matches 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1122 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: RECEPTOR ANUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E
CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: COCUZZO, Anna L.
REGISTRATION NUMBER: 42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatibl
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for V
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 732-594-1273
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                                                                                                  492
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nes 290; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                  GCTGGTGGTGTCCGCGAGCTGCGCACCACCACCACCTCTACCTGTCCAGCAT 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGCACGAGAACGGCACCGACCCTTGGGACACCAACGAGTGCCGCCCCCACCGAGTTTGC
                                CAAGTTCCACTACTTCCCCAATGGGTCCCTGGTCCCAGGTTCGGCCACCTGTACGGTCAT
                                                                                                                                                                                                                                                                                                                                                   GCCGGTCTCTGACCTCCTGGTCCTGGTCCTTGGAATGCCCCCTGGAGGTCTATGAGATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCGTCATCTGGGCCGTGGCCTTCTGCAGCGCCCGGGCCCATCTTCGTGCTAGTCGGGGT
                                                                                                CGGCATCGTCTGGGGCTTCTCCGTGCTCTTCTCCCTGCCCAACACCAGCATCCATGGCAT 551
                                                                                                                                                                                                  GAGCTGCACCTACGCCACGGTGCTCACCATCACAGCGCTGAGCGTCGAGCGCTACTTCGC
                                                                                                                                                                                                                                 GACCGTGTGCTTCGCCTCCATCCTCAGCATCACCGTCAGCGTGGAGCGCTACGTGGC 431
                                                                                                                                                                                                                                                                  GCAGTACCGGCCCTGGAACTTCGGCGACCTCCTCTGCAAACTCTTCCAATTCGTCAGTGA
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                                                                                                                                                                                                                                                                                                                                GGCCTTCTCCGAT----CTGCTCATCTTCCTCTGCATGCCCCTGGACCTCGTTCGCCTCTG
                                                                                                                                 CATCTGCTTCCCACTCCGGGCCAAGGTGGTGGTCACCAAGGGGCGGGTGAAGCTGGTCAT
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FastSEQ for Windows Version
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                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 302; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: COCUZZO, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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APPLICANT: Van Der Ploeg, Leonardus H.T.
                               252 GGCGGTCTCTGACCTCCTGGTCCTGCTCCTTGGAATGCCCCTGGAGGTCTATGAGATGTG 311
                                                                                                                                                          132 CGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGGTCATTGGCAATGTCCTGGTGTG 191
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FILING DATE: 3-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
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                                                                 GCTGGTAGTGTCACGCTTCCGCGAGATGCGCACCACCACCAACCTCTACCTGTCCAGCAT 216
                                                                                           CCTGGTGATTCTGCAGCACCAGGCTATGAAGACGCCCACCAACTACTACCTCTTCAGCCT 251
                                                                                                                              CGTCACCGCCACCTGCGTGGCGCTCTTCGTGGTGGGTATCGCGGGCAACCTGCTCACGAT 156
    GGCCTTCTCCGACCTAC---TCATCTTCCTCTGCATGCCCCTCGACCTCTTCCGGCCTCTG
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Feighner,
                                                                                                                                                                                               Conservative
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                                                                                                                                                                                          Score 114; DB 4; L
Pred. No. 1.1e-16;
0; Mismatches 270;
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US-09-077-675A-4
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APPLICANT: Pai, Lee
APPLICANT: Feighner
APPLICANT: Howard,
APPLICANT: Pong, SI
APPLICANT: Van Der
                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      FILING DATE: 3-JUN-1:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Cocuzzo, Anna L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 07065-0900
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                                                                              TELEFAX:
                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: P.O. CITY: Rahway
                LENGTH:
                                                              TELEX:
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nucleic acid
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              1029 base pairs
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Howard, Andrew D.
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Sequence 4, Application US/09077675A Patent No. 6242199
                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,675A
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19590P
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; STRANDEDNESS: Sil; TOPOLOGY: linear; MOLECULE TYPE: CDN:
US-09-077-675A-4
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US-08-086-439C-2
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                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                     APPLICANT: Chio, Christopher L.
APPLICANT: Huff, Rita M.
TITLE OF INVENTION: A Synthetic Gene
TITLE OF INVENTION: Receptors
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 CGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGTCATTGGCAATGTCCTGGTGTG 191
                                                                                                       CITY: Kalamazoo
                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 52.1 nes 301; Conservative
                                                                                                                                 ADDRESSEE: The Upjohn Company, Corp. ADDRESSEE: Property Law
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCTGTCTTCTGCCTCACTGTGCTCTATAGCCTCATCG
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 Patentin Release #1.0,
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52.1%;
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Pred. No. 2.4e-16;
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Mismatches 271;
 Version #1.25
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                                                                                                                                                                                    RESULT 8
                                                                                                                             Sequence 2, Application US/08434877 Patent No. 5721132 GENERAL INFORMATION:
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Best Local
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TELEX: 224401
INFORMATION FOR SEQ ID NO:
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NAME: Darnley Jr., James D.
REGISTRATION NUMBER: 3,673
REFERENCE/DOCKET NUMBER: 4700
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-385-5210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1161 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 435
                                                 CORRESPONDENCE ADDRESS
                                                                                                     APPLICANT: Chio, Christopher APPLICANT: Huff, Rita M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1: MOLECULE TYPE:
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STREET:
CITY: K
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Kalamazoo
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TITLE OF INVENTION: A Synthetic Gene TITLE OF INVENTION: Receptors NUMBER OF SEQUENCES: 9
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ADDRESSEE: The Upjohn Company, ADDRESSEE: Property Law STREET: 301 Henrietta Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGACCTCCTGGTCCTGCTCCTTGGAATGCCCCTGGAGGTCTATGAGATGTGGCGCAAC
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                                               Corp.
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                                                  Intellectual
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US-08-475-742-3
; Sequence 3, Application US/08475742
; Patent No. 6121015
; GENERAL INFORMATION:
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Best Local Similarity
Matches 236; Conserv
APPLICANT: O'Malley, Karen APPLICANT: Todd, Richard D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 224401
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 33,673
REFERENCE/DOCKET NUMBER: 4700 DV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-385-5210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/434,877
FILING DATE: 1 July 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Darnley Jr., James D.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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Pred. No. 2.5e-16;
0; Mismatches 206;
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RESULT 10
US-08-056-051-1
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Best Local Similarity 53.4%;
Matches 236; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Gene Encoding the Rat Dopamine FILE REFERENCE: WU 102 CON DIV. CON TOUR CORRENT APPLICATION NUMBER: US/08/475,742 CURRENT FILING DATE: 1995-06-07 EARLIER APPLICATION NUMBER: US 08/261,293 EARLIER FILING DATE: 1994-06-16 EARLIER APPLICATION NUMBER: US 08/014,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER FILING DATE: 1993-01-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS: Van tol, H. H.
AUTHORS: Bunzow, J. R.
TITLE: Cloning of the gene for a human dopamine D4 receptor
TITLE: with high affinity for the antipsychotic clozapine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (1)...(1367)
OTHER INFORMATION: D4 Dopamine Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAGES: 610-614
DATE: 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL: Nature VOLUME: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
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                                                                         638 GGCCGCGACCCCGCCGTGTGCC 659
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                                                                                                              CACTACTTCCCCAATGGGTCCC
                                                                                                                                                                           GTCTGGGGCTTCTCCGTGCTCTTCTCCCTGCCCAACACCAGCATCCATGGCATCAAGTTC
                                                                                                                                                                                                                                                     CACCCGTTCCGCCCAAACTGCAGAGCACCCCGGCGCCCTCAGGATCCTCGGCATC
                                                                                                                                                   ACGTGGCTGCTGTCCGCGGCGGTGGCGCGCGCGTACTGTGCGGCCTCAACGACGTGCGC
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Pred. No. 2.5e-16;
0; Mismatches 206
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Sequence 1, Application US/08056051 Patent No. 5516683 GENERAL INFORMATION:

APPLICANT:

Grandy,

David James

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/056, FILING DATE: 19930429 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: NAME: NO. 5516683nan, Kevin EREGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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LENGTH: 1370 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: A No. 55166
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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GTGCCGCTGCGCTACAACCGGCAGGGTGGGAGCCGCCGGCAGCTGCTGCTCATCGGCGCC
                       CACCCGTTCCGCGCCAAACTGCAGAGCACCCGGGCCCCGGGCCCTCAGGATCCTCGGCATC 498
                                                                                                                                                                     TACCCTTTCTTGTTCGGGCCCCGTGGGCTGCTACTTCAAGACGGCCCTCTTTGAGACCGTG 378
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                                                                                                                                                                                                                                                                           GTGGCCACCGAGCGCCCCTGCAGACGCCCACCAACTCCTTCATCGTGAGCCTGGCGGCC
                                                                                                                                                                                                                                                                                                                                             TGCACCGCCTCCATCTTCAACCTGTGCGCCATCAGCGTGGACAGGTTCGTGGCCGTGGCC 517
                                                                                                  TGCTTCGCCTCCATCCTCAGCATCACCACCGTCAGCGTGGAGCGCTACGTGGCCATCCTA 438
                                                                                                                                      GGCGCGTGGCTGAGCCCCCGCCTGTGCGACGCCCTCATGGCCATGGACGTCATGCTG
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10 South Wacker Drive, Suite 3000
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Pred. No. 2.5
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2.5e-16;
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RESULT 11
US-07-928-611-17
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Best Local :
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APPLICANT: Van Tol, Hubert |
APPLICANT: Civelli, Olivier
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TELEX: 810-221-8317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: No. 556960lnan, Kevin
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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NAME/KEY:
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                 199 ATTCTGCAGCACCAGGCTATGAAGACGCCCACCACTACTTACCTCTTCAGCCTGGCGGTC 258
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278 GTGGCCACCGAGCGCCCTGCAGACGCCCACCAACTCCTTCATCGTGAGCCTGGCGGCC
                                                                                                                                                                                                                NAME/KEY:
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CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                al Similarity
236; Conserv
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10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                             1370 base pairs
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                                                                                                                              Score 112.4; DB 1;
Pred. No. 2.5e-16;
0; Mismatches 206;
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                                                                                                                                 Indels
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1370 base pairs
1.ENGTH: 1370 base pairs
               FEATURE:
                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: NO. 5883226nan, Kevin
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Civelli, Olivier
APPLICANT: Van Tol, Hubert H.M.
TITLE OF INVENTION: A NO. 5883226el Human Dopamine
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                 FEATURE:
                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 07-JUN CLASSIFICATION: 53(
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pain
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COUNTRY:
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                                                                                LOCATION:
                                                                                                  NAME/KEY:
                                                                                                                                                  TOPOLOGY:
                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                              TYPE: nucleic acid
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CDS
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RESULT 13
US-09-060-694-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/09060694 Patent No. 6203998 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 236; Conserv
              TELECOMMUNICATION INFORMATION: TELEPHONE: 312-913-0001
                                           ATTORNEY/AGENT INFORMATION:
NAME: NO. 6203998nan, Kevin
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Van Tol, Hubert H.M.
TITLE OF INVENTION: A No. 6203998el Human Dopamine Receptor and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Civelli, APPLICANT: Van Tol,
                                                                                                                                                                                                                                                                 COUNTRY: US
                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    638 GGCCGCGACCCCGCCGTGTGCC
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TELEFAX:
                                                                                                                               APPLICATION NUMBER: FILING DATE: 15-APR
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                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                STREET: 300 Sc
CITY: Chicago
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Pred. No. 2.5e-16;
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US-09-378-074-17
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US-09-060-694-17
                                                                                                                                                                                                                              Sequence 17, Application US/09378074 Patent No. 6437114 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uery Match 15.4%; est Local Similarity 53.4%; datches 236; Conservative
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LENGTH: 1370 base pairs
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NAME/KEY:
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LOCATION:
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                            TITLE OF INVENTION: A NO. 6437114el Human Dopamine Receptor NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                             APPLICANT: Van Tol, Hubert H.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACCCGTTCCGCGCCAAACTGCAGAGCACCCGGCGCCGCGGCCCTCAGGATCCTCGGCATC 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCACCGCCTCCATCTTCAACCTGTGCGCCATCAGCGTGGACAGGTTCGTGGCCGTGGCC
                                      COUNTRY: USA
ZIP: 60606
                                                                       CITY: Chicago
STATE: Illinois
                                                                                                   ADDRESSEE: Allegretti & Witcoff, Ltd. STREET: 10 South Wacker Drive, Suite 3000
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Pred No. 2.5e-16;
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Best Local Similarity
Matches 236; Conserv
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                    638
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APPLICATION NUMBER: 07/928,611
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6437114nan, Kevin E
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                      ACGTGGCTGCTGTCCGCGGCGGTGGCGGCGCCCGTACTGTGCGGCCTCAACGACGTGCGC
                                                                                                                       GTCTGGGGCTTCTCCGTGCTCTTCTCCCTGCCCAACACCAGCATCCATGGCATCAAGTTC
                                                                                                                                                          GTGCCGCTGCGCTACAACCGGCAGGGTGGGAGCCGCCGGCAGCTGCTGCTCATCGGCGCC
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STRANDEDNESS: single
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53.4%; Pred. No. 2.5e-16;
tive 0; Mismatches 206
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Search completed: January 17, 2003, 02:35:14 Job time: 61 secs
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PCT-US93-07370-17
; Sequence 17, Applicat
; GENERAL INFORMATION:
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Matches 236; Conserv
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LENGTH: 1370 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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LOCATION:
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APPLICANT:

APPLICANT:

TITLE OF INVENTION: A Novel Human Dopamine Receptor and Uses NUMBER OF SEQUENCES: 22

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
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1263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                       // SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT: *
// SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT: *
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Copyright (c) 1993 - 2003 Compus
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Amino acid sequenc	AAG63353	22	415	99.1	1252	10
Human neurotensin-	AAY52992	21	415	99.1	1252	9
Human G protein co	AAB02830	21	415	99.1	1252	000
Human orphan G pro	AAY71296	21	415	99.1	1252	7
Amino acid sequenc	AAB67805	22	412	99.1	1252	0
Amino acid sequenc	AAB67803	22	412	99.1	1252	ъ
Splice variant of	AAB67806	22	296	99.1	1252	4
Splice variant of	AAB67807	22	293	99.1	1252	ω
Human nGPCR15. Ho	AAG80937	22	249	99.1	1252	N
Amino acid sequenc	AAB68333	22	242	100.0	1263	щ.
Description	ID	DB	Query Match Length DB	Query Match	Score	Result

Long form of motil	AAB6265	22	412	26.4	333	4.5
Amino acid sequenc		21	412	26.4	333	44
Human G prot		21	412	26.4	333	43
form		22	386	26.4	333	42
		21	386	26.4	333	41
	AAU3898	22	660		337	40
	ABB7168	22	660	6	337	39
	AAU3898	22	595	7.	352	38
	ABB7169	22	595	7.	352	37
	AAU3896	22	428	ω.	418	36
Drosophila melanog	ABB6475	22	428	ω ·	418	35
D. melanogaster	AAB8696	22	419	ω.	418	34
ne	AAB9918	22	405	7	596	33
Mouse growth	AAY4464	21	405	7.	596	32
-prote	AAE0363	22	439	0	642	31
Ξ	AAB9919	22	412	0	642	30
Rat G-protein coup	AAE0363	22	413	1.	646	29
Human G-protein	AAE1563	23	426	ω.	-	28
Human novel cytoki	AAU6856	22	445	ω.	~1	27
	AAU6852	22	445	ω	-1	26
	AAE0362	22	426	53.9	680.5	25
	AAB9918	22	403	ω	\sim	24
growth	AAY4464	21	403	ω.		23
E E	AAY9067	21	403	ω		22
a	AAY9063	21	403	ω		21
	AAE1426	23	395	1.	(.)	20
	AAE0363	22	395	۲.	1.1	19
acid s	AAG6336	22	395	1.	4.1	18
Human NMUR2 prote	AAE1426	23	415	9.	K. 3	17
-pro	AAU7715	23	415	99.1	1252	16
Amino acid sequenc	AAB6780	22	415	99.1		15
Amino acid sequenc	AAB6780	22		9.	ĸ.	14
G-pr	AAE0362	22	415	99.1	1252	13
P-bi	AAG64297	22	415	99.1	K.	12
Amino acid sequenc	AAG6336	22	415	99.1	1252	11

ALIGNMENTS

AAB68333 RESULT 1 G-protein coupled receptor; obesity; signal transduction; diabetes; metabolic disease; neurological disease; psychotherapy; dermatology; urogenital disease; inflammation; cancer; tissue repair; photoageing; skin pigmentation; frailty; osteoporosis; cardiovascular disease; gastrointestinal disease; infection; allergy; respiratory disease; sensory organ disorder; sleep disorder; hair loss; gene therapy; (PFIZ) PFIZER LTD (PFIZ) PFIZER INC 08-OCT-1999; 06-OCT-2000; 2000EP-0308852. 11-APR-2001 EP1090990-A1 Amino acid sequence of human g-protein coupled receptor PFI-002. 09-JUL-2001 AAB68333; AAB68333 standard; Protein; 242 Harland L; Homo sapiens (first entry) 99GB-0023888 A

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RESULT 2
AAG80937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                         G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder;
WO200136473-A2
                                                                                                                                            cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer attention deficit-hyperactivity disorder/attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a human G-protein coupled receptor. The G-protein coupled receptor polynucleotide and polypeptide are useful as pharmaceuticals or in the manufacture of medicaments for the treatment of obesity. They are useful in the diagnosis and treatment of diseases and disorders associated with signal transduction such as obesity, diabetes and metabolic disease, neurological disease, psychotherapeutics, urogenital disease, inflammation, cancer, tissue repair, dermatology, skin pigmentation, photogeing, frailty, osteroprofile additional processing and processing of the process of 
                                                                                                                                                                                                                                                                                                                                                                      Human nGPCR15
                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG80937 standard; Protein; 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         osteoporosis, cardiovascular disease, gastrointestinal disease, infection, allergy and respiratory disease, sensory organ disorders, sleep disorders and hair loss. The polynucleotide may also by useful
                                                                                                      neuroprotective
                                                                                                                            rheumatoid arthritis; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human G-protein coupled receptor (GPCR) polynucleotides and polypeptides, for screening modulators of the polypeptide useful in treating diseases associated with signal transduction, e.g. cancer, inflammation, or especially, obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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N-PSDB; AAF85107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLVCLVILQHQAMKTFTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEKLQNASWIYQQKLEDFFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242;
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42; Conservative
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Pred. No. 1e-142;
Mismatches (
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                                                                                                                              disorder;
                                                                                                                            respiratory
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                                                                                                                                                                                                                                                                                   tailure;
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Qy DЪ ρy Db Qy

> ω ш

MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN

Best Loc Matches Query Match

Local

Similarity

99.1%;

Score 1252; DB 22; Pred. No. 2.3e-141; Mismatches

Length Indels

249;

0,:

Gaps

0

60

62

240;

Conservative

Вþ

123 121 63 61

ALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS

180

120

122

VLVCLVILQHQAMKTPNTYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKT VLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKT

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28-DEC-1999;
22-FEB-2000;
28-FEB-2000;
28-FEB-2000;
02-MAR-2000;
03-MAR-2000;
09-MAR-2000;
17-MAR-2000;
21-MAR-2000;
21-MAR-2000;
02-MAY-2000;
08-MAY-2000;
                                                                    treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-hyperactivity disorder/attention deficit disorder), and neuronal disorders such as Alzheimer's disease, Parkinson's disease migraine and senile dementia. Additional disorders include inflammatory
                                                                                                                                                disorder affecting the brain or a genetic predisposition, specifically schizophrenia. ngPCRx are useful for identifying compounds useful for treating schizophrenia. Detection of ngPCRx in a sample is useful as a diagnostic tool for diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1, metabolic and cardiovascular diseases, proliferative disorders and
                                        conditions (e.g. Cradisorders, cancers,
                                                                                                                                                                                                                                           The present invention relates to novel G protein-coupled receptors (nGPCRX; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is one such G protein-coupled receptor. GPCRs are also known a seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful for screening a human to diagnose a diagnose receptors are useful for screening a human to diagnose a
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vogeli G,
Schellin
                                                                                                                                                                                                                                                                                                                                                         Claim 37; Page
                                                                                                                                                                                                                                                                                                                                                                                      New G protein-coupled polynucleotide useful
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-389826/41.
N-PSDB; AAH50977.
                                                                                                                                   hormonal disorders. Modulators of nGPCRx activity have the utility for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-NOV-1999;
17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PHAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHARMACIA &
                         ns (e.g. Crohn's disease), rheumatoid arthritis, s, cancers, respiratory ailments such as asthma, e.g. inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KA,
249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wood
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2000US-0185421.
2000US-0185554.
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2000US-0190310.
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2000US-0186811.
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2000US-0203111
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2000US-0198568
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99US-0173396.
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99US-0166071
                                                                                                                                                                                                                                                                                                                                                         261pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ПРЈОНИ СО
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parodi LA,
PS, Bannig
                                                                                                                                                                                                                                                                                                                                                                                 receptor (nGPCR-x) and its encoding for diagnosing and treating e.g. schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bannigan CM,
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Ruff V,
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Sejlitz T, Huf
                                        and inflammatory
                                                          autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huff RM;
                                                                                       disease,
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RESULT 3
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           dysfunctions or diseases. These diseases include peripheral nervous system, psychiatric and central nervous system disorders (e.g. schizophrenia, episodic parcaysmal anxiety, phobia, Parkinson's disease, migraine, epilepsy, bulinia or stroke), cardiovascular disease (e.g. heart failure, angina pectoris, myocardial infarction or hypertension), dyslipidemias, obesity, emesls, gastrointestinal disorders (e.g. inflammatory bowel disease or motility disorders), osteoporosis, inflammatory bowel disease or motility disorders), path, cancers, immune disorders, allergies, sepsis or gynecological disorders. Agonists or antagonists of IGS4 are effective with regard to disorders of the nervous system, including the central and peripheral nervous systems, disorders of the gastrointestin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-1999;
24-SEP-1999;
28-JUL-2000;
31-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human: G-protein coupled receptor; IGS4; IGS4A; IGS4B; schizophrenia; nervous system disorder; psychiatric disorder; Parkinson's disease; episodic paroxysmal anxiety; phobia; migraine; epilepsy; bulimia; strc cardiovascular disease; heart failure; angina pectoris; obesity; emes; motility disorder; myocardial infarction; hypertension; dyslipidemia; gastrointestinal disorder; inflammatory bowel disease; osteoporosis; inflammation; infection; pain; cancer; immune disorder; allergy; sepsi
                                                                                                                                                                                                                The present sequence represents a splice variant of the short version a human G-protein coupled receptor designated IGS4A. IGS4 exists in typolymorphic forms, IGS4A and IGS4B. The IGS4 receptors and IGS4
                                                                                                                                                                                    polynucleotides are useful for predysfunctions or diseases. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gynecological
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                                                                                                                                                                                                                                                                                  Example 1b;
                                                                                                                                                                                                                                                                                                                                                useful
                                                                                                                                                                                                                                                                                                                                                           New G-protein coupled receptors and the
                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAF80327
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   cardiovascular system,
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                                                                                                                                                                                                                                                                                                                              cardiovascular diseases,
                                                                                                                                                                                                                                                                                                                                           preventing, ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 99NL-1013140.
; 2000EP-0202683.
; 2000US-0222047.
                                                                                                                                                                                                                                                                             Page 96-97; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-EP09584
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   skeletal
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 thyroid,
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gastrointestinal lung or
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Best Local
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                                                                                                                                                                                 24-SEP-1999;
24-SEP-1999;
28-JUL-2000;
31-JUL-2000;
                                          New G-protein coupled receptors and useful for preventing, amellorating disorders, cardiovascular diseases,
                                                                                                                                                                                                                                                                                                                                                       Human; G-protein coupled receptor; IGS4; IGS4A; IGS4B; schizophrenia; nervous system disorder; psychiatric disorder; Parkinson's disease; episodic paroxysmal anxiety; phobia; migraine; epilepsy; bulimia; stroke; cardiovascular disease; heart failure; angina pectoris; obesity; emesis; motility disorder; myocardial infarction; hypertension; dyslipidemia; gastrointestinal disorder; inflammatory bowel disease; osteoporosis; inflammation; infection; pain; cancer; immune disorder; allergy; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genitourinary system, or immunological disease. are useful as diagnostic reagents for detecting overexpression or altered expression of IGS4.
                                   or cancers
                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                              gynecological
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Splice variant of G-protein coupled receptor IGS4A long version.
                                                                                                                                                                                                                                              25-SEP-2000; 2000WO-EP09584.
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                                                                                              2001-273568/28
)B; AAB80326.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKT
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                                                                                                                                                          SOLVAY PHARM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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                                                                                                                                                                                 2000EP-0202683
2000US-0222047
                                                                                                                                 Σ,
                                                                                                                                                                                                                                                                                                                                               disorder
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                                                                                                                                 Berger
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99.6%;
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Pred.
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No. 2
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                                          the polynucleotides encoding or correcting nervous system dyslipidemias, inflammations,
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                                                                                                                                 Nys
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Example

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92-93;

English

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RESULT 5
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   24-SEP-1999;
24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                       gynecological
                                                                                                                                                                                                                                                                                                                                                                                                                                                   nervous system disorder; psychiatric disorder; Parkinson's disease; episodic paroxysmal anxiety; phobia; migraine; epilepsy; bulimia; stroke; cardiovascular disease; heart failure; angina pectoris; obesity; emesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of G-protein coupled receptor IGS4A short version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypertension), dyslipidemias, obesity, emesis, gastrointestinal disorders (e.g. inflammations bowel disease or mothlity disorders), osteoporosis, inflammations, infections (e.g. bacterial, fungal, protozoan or viral), pain, cancers, immune disorders, allergies, sepsis or gynecological disorders. Agonists or antagonists of IGS4 are effective with regard to disorders of the nervous system, including the central and peripheral nervous systems, disorders of the gastrointestinal system, cardiovascular system, skeletal muscle, thyroid, lung or genitourinary system, or immunological disease. The IGS4 polynucleotides are useful as diagnostic reagents for detecting under-expression, overexpression or altered expression of IGS4.
                                                                                                                                                           12-APR-2001
                                                                                                                                                                                                              WO200125269-A2
                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; G-protein
                                                                                            25-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB67803 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a splice variant of the long version of human G-protein coupled receptor designated IGS4A. IGS4 exists in two polymorphic forms, IGS4A and IGS4B. The IGS4 receptors and IGS4 polynucleotides are useful for preventing, ameliorating or correcting dysfunctions or diseases. These diseases include peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (e.g. heart failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKT
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239; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                            2000WO-EP09584.
                                                                                                                                                                                                                                                                                                                                       disorder
99EP-0203140
99NL-1013140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coupled receptor; IGS4; IGS4A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.1%;
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGS4B; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     These diseases include peripheral nervous system, psychiatric and central CC nervous system disorders (e.g. schizophrenia, episodic paroxysmal CC anxiety, phobia, Parkinson's disease, migraine, epilepsy, bulimia or cystroke), cardiovascular diseases (e.g. heart failure, angina pectoris, CC myocardial infarction or hypertension), dyslipidemias, obesity, emesis, cg qastrointestinal disorders (e.g. inflammatory bowel disease or motility CC disorders), osteoporosis, inflammations, infections (e.g. bacterial), CC fungal, protozoan or viral), pain, cancers, immune disorders, allergies, csepsis or gynecological disorders of the nervous system, including the CC entral and peripheral nervous systems, disorders of the gastrointestinal csystem, cardiovascular system, or immunological disease. The IGS4 polynucleotides are useful as diagnostic reagents for detecting under-expression, coverexpression or altered expression of IGS4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
      nervous system disorder; psychiatric episodic paroxysmal anxiety; phobia;
                                    Human; G-protein coupled receptor; IGS4; IGS4A; IGS4B; schizophrenia;
                                                                         Amino acid
                                                                                                                                                                    AAB67805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents the short version of a human G-procoupled receptor designated IGS4A. IGS4 exists in two polymorphic IGS4A and IGS4B. The IGS4 receptors and IGS4 polynucleotides are under the control of the IGS4 receptors and IGS4 polynucleotides are under the IGS4B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New G-protein coupled receptors and useful for preventing, ameliorating disorders, cardiovascular diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 81-82; 102pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or cancers
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31-JUL-2000;
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                                                                                                                                                                                                                                            VLVCLVILOHQAMKTPTNYYLFSLAVSDLLVLLLLGMPLEVYEMWRNVPFLFGPVGCYFKT 120
                                                                                                                                                                                                                                                                                                           ALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS
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DB; AAF80323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                      standard;
                                                                   sequence of G-protein coupled receptor IGS4B short version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   412 AA;
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                                                                                                     (first entry)
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2000US-0222047
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                                                                                                                                                                  Protein;
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        phobia; migraine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1252; DB 22;
Pred. No. 4.4e-141;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loeken C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the polynucleotides encoding or correcting nervous system dyslipidemias, inflammations
                       disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nys
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Parkinson's disease;
epilepsy; bulimia; stroke;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                     γΩ
                                                                                                                                                                                                                                                                                                                                                                                                        for preventing, ameliorating or correcting dysfunctions or diseases.

C These diseases include peripheral nervous system, psychiatric and central nervous system disorders (e.g. schizophrenia, episodic paroxysmal central canxiety, phobia, Parkinson's disease, migralne, epilepsy, bulimia or stroke), cardiovascular diseases (e.g. heart failure, angina pectoris, myocardial infarction or hypertension), dyslipidemias, obesity, emesis, castrointestinal disorders (e.g. inflammatory bowel disease or motility disorders), osteoporosis, inflammations, infections (e.g. bacterial, fungal, protozoan or viral), pain, cancers, immune disorders, allergies, ceffective with regard to disorders agonists or antagonists of IGS4 are ceffective with regard to disorders of the nervous system, including the central and peripheral nervous system, disorders of the gastrointestinal central and peripheral nervous system, disorders of the gastrointestinal central and peripheral nervous system, disorders of the gastrointestinal constitution or immunological disease. The IGS4 polynucleotides are useful as diagnostic reagents for detecting under-expression, concerns as a constitution or alternal expression of IGS4.
                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 239
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24-SEP-1999;
28-JUL-2000;
31-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New G-protein coupled receptors and the polynucleotides encoding tuseful for preventing, ameliorating or correcting nervous system disorders, cardiovascular diseases, dyslipidemias, inflammations,
                                                                                                                                                                                                                                                                                                                                                                                                overexpression or altered expression of IGS4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiovascular disease; heart failure; angina pectoris; obesity; emesis; motility disorder; myocardial infarction; hypertension; dysilpidemia; gastrointestinal disorder; inflammatory bowel disease; osteoporosis; inflammation; infection; pain; cancer; immune disorder; allergy; sepsis;
                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                           MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN 60
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                     IHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRV
                                                                                                                                                       VLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKT 120
                                                        ALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRALRILGIVWGFSVLFSLPNTS
                                                                                            ALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS
                                                                                                                               VLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKT
                                                                                                                                                                                                          MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN
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Page
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99NL-1013140.
2000EP-0202683.
2000US-0222047.
                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                      99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102pp; English.
                                                                                                                                                                                                                                                                                                      Score 1252; DB 22; Pred. No. 4.4e-141;
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RESULT
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01-OCT-1999;
01-OCT-1999;
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28-MAY-1999;
28-MAY-1999;
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28-MAY-1999;
28-MAY-1999;
29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-1999;
12-MAR-1999;
12-MAR-1999;
The present amino acid sequence is the hRUP6, an endogenous human orphan G protein-coupled receptor (GPCR). The full length hRUP6 cDNA was cloned by RT-PCR using human thymus cDNA as template. The orphan GPCR of the invention, like all GPCRs has seven transmembrane alpha helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR agonists and antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue localisation expression analysis to provide information about their
                                                                                                                                                                                                                                                                                                                                                                                                                                  29-SEP-1
29-SEP-1
29-SEP-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; orphan G protein-coupled receptor transmembrane receptor; signal cascade.
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                                                                                                                                                                                                                  Novel human orphan G
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16-FEB-1999
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                                                                                                                                                                                                    uman orphan G protein-coupled receptors and the encoding cDNAs in the identification of G protein-coupled receptor agonists
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                                                                                                                                                                                                                                            AAD01123
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37-JUG 1999
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29-SEP-1999;
29-SEP-1999;
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identification; agonist; screening; therapeutic; pharmaceutical;
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990S-0137131.
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990S-0141448.
990S-0151114.
990S-0152524.
PHARM
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Pred. No. 4.5e-141;
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Best Local Similarity
Matches 239; Conserv
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                  Ahmad S,
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RESULT 10
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Best Local S
Matches 239
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24-FEB-2000; 2000JP-0052252.
30-MAR-2000; 2000JP-0097896.
19-JUN-2000; 2000JP-0187536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a human G-protein coupled receptor neurotensin-like receptor (NLR). The NLR polynucleotide and protein can be used to isolate compounds that bind, (ant)agonise or alter the activity or expression of the NLR. The NLR is a G-protein coupled receptor which is expressed in the central nervous system and shares homology with human neurotensin receptor. The receptors can be used in assays to identify agents for producing anasthesia and analgesia.
                      WPI; 2001-488917/53.
N-PSDB; AAH43072.
                                                                                                                                                                                                                                                                                                                   AAG63353 standard;
  Identifying
                                                   Okubo
                                                               Hinuma
                                                                                                                                                      02-FEB-2001;
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                                                                                                                                                                                                                                     TGR-1;
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                                                                                 (TAKE
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                                                                                                                                                                                                                                                        Amino acid sequence
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Pred. No. 4.5e-141;
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or more members
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Best Local (
                                                                                                                                                04 - FEB - 2000;
24 - FEB - 2000;
30 - MAR - 2000;
19 - JUN - 2000;
                                                              WPI; 200
      Identifying predicted or actual structures of two chemical or physical library by mass spectrometry correlating molecular mass measurements of two or shared chemical history -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a human TGR-1 protein. The specification describes a method of screening a compound, which is capable of binding properties of neuromedin U to TGR-1. The method is useful for screening preventatives and remedies for hypertension, stress diseases, etc.. TGR-1 antagonists are also useful for treating the same diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chemical or physical library by mass spectrometry comprising correlating molecular mass measurements of two or more members with
                                                                                             Okubo
                                                                                                        Hinuma
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                                                                                                                                                                                                                                             WO200157524-A1
                                                                                                                                                                                                                                                                                      TGR-1; neuromedin
                                                                                                                                                                                                                                                                                                                                                     AAG63366;
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»B; AAH43075.
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                                                                                                      Shintani
                                                                                                                                               ; 2000JP-0032773.
; 2000JP-0052252.
; 2000JP-0097896.
; 2000JP-0187536.
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99.6%;
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Pred. No. 4.5e
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1.5e-141;
                                                                                                      72,
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                            or more members comprising
                   more
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RESULT 12
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Best Local Sim
Matches 239;
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31-MAR-2000;
23-MAY-2000;
               The
triphosphate (GTP)-binding protein-coupled receptor.
                                    Claim 1; Pages 100-103; 137pp; Japanese
                                                                     Family of guanosine triphosphate binding protein genes encoding them for treatment and prevention
                                                                                                              N-PSDB;
                                                                                                                                                  Matsumoto S,
Sugiyama T;
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                                                                                                                                                                                                                                                            28-DEC-2000;
                                                                                                                                                                                                                                                                                                             WO200148189-A1
                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                       muscular; urinary;
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                                                              these receptors
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                                                                                                                                                                                                            ; 99JP-0375152.
; 2000JP-0101339.
; 2000JP-0155978.
                                                                                                                                                                                                                                                                                                                                                                  protein-coupled receptor; neuroprotective; immunomodulatory;
rinary; circulatory; anorectic; human; guanosine triphosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page
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             protein sequence
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Pred. No. 4.5e
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RESULT 13
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                                                                                                                                                                                                                                                                                                                NMU; inflammation; arthritis; autoimmune disease; septicaemia; psychotic; mental retardation; transplant rejection; neurological disorder; anxiety; respiratory disorder; depression; schizophrenia; dementia; obestity; pain; gastrointestinal disorder; hypertension; hypotension; epilepsy; diabetes; ischaemia; stroke; cancer; sexual disorder; circadian disorder; anorexia; dermatological; psoriasis; Parkinson's disease; nausea; bulimia; allergy; Alzhelmer's disease; AIDS; hormonal disorder; memory disorder; migraine; cardiovascular disorder; renal disorder; bone disease; delirium; asthma; cardiovascular disorder; renal disorder; bone disease; delirium; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for the investigation, diagnosis, treatment and prevention o diseases associated with GTP-binding protein-coupled receptors, incurrence neurological, circulatory, digestive system, immune system, muscle urinary system disorders. GTP-binding proteins are also known as
                         WO200144297-A1
                                                                                                             Domain
                                                                                                                                      Domain
                                                                                                                                                                Domain
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                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                           Cushing's disease; dysmenorrhoea; antianginal; cytostatic; osteoporosis; metabolic disorder; behavioural disorder; Addison's disease; dyskinesia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE03629 standard;
                                                                                     Domain
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                                                                                                                                                                                                                                                                                tranquiliser;
                                                                                                                                                                                                                                                                                                                                                                                                                Human; G-protein coupled receptor; SNORF72; neuromedin U neuropeptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human G-protein coupled receptor, SNORF72.
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215..240
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99.6%;
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Pred No 4.5e-141;
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                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders, ischaemia, stroke, cancers, sexual disorders, circadian disorders, renal disorders, bone diseases including osteoporosis, benign prostatic hypertrophy, gastrointestinal disorders, nasal congestion, dermatological disorders such as psoriasis, allergies, Parkinson's disease, Alzheimer's disease, acute heart failure, angina disorders, delirium and dyskinesias such as Huntington's disease. They can also be used to regulate steroid hormone disorders, epinephrine release disorders, electrolyte balance disorders, epinephrine disorders, memory
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A purified mammalian SNORF62 or SNORF72 receptor protein for identification of compounds to treat e.g. inflammation, arthritis, autoimmune diseases, transplant rejection, AIDS, cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Fig 4; 256pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence
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                                                                                                                                                                                                                                                    MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN 60
IHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRL
                  IHGIKPHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRV
                                                                             ALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS
                                                                                               ALFETYCFASILSITTYSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-390240/41.
                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               so, drug addiction, migraine, Addison's disease, Cushing's prevent miscarriage, induce labour or to treat dysmenorrhoea ent sequence is human G-protein coupled receptor, SNORF72.
                                                                                                                                                                                                                                                                                                                                                                                               415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         somatosensory disorders, metabolic disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0466435.
2000US-0558099.
2000US-0609146.
                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                             Score 1252; DB 22;
Pred. No. 4.5e-141;
1; Mismatches 0;
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243
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RESULT 14 AAB67802

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1 MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN 60 MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN

Matches

Conservative

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Indels

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Gaps

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Query Match
Best Local Similarity
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24-SEP-1999;
28-JUL-2000;
31-JUL-2000;
                                                                                                                                                                               These diseases include peripheral nervous system, psychiatric and central nervous system disorders (e.g. schizophrenia, episodic paroxysmal anxiety, phobia, Parkinson's disease, migraine, epilepsy, bulimia or stroke), cardiovascular diseases (e.g. heart failure, angina pectoris, myocardial infarction or hypertension), dyslipidemias, obesity, emesis, gastrointestinal disorders (e.g. inflammatory bowel disease or motility disorders), osteoporosis, inflammatory bowel disease or motility disorders), osteoporosis, inflammations, infections (e.g. bacterial, fungal, protozoan or viral), pain, cancers, immune disorders, allergies, sepsis or gynecological disorders of the nervous system, including the central and peripheral nervous systems, disorders of the gastrointestinal
                                                                                                                       central and peripheral nervous systems, disorders of the gastrointestina system, cardiovascular system, skeletal muscle, thyroid, lung or genitourinary system, or immunological disease. The IGS4 polynucleotides are useful as diagnostic reagents for detecting under-expression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New G-protein coupled receptors and the polynucleotides encoding useful for preventing, ameliorating or correcting nervous system disorders, cardiovascular diseases, dyslipidemias, inflammations,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nervous system disorder; psychiatric disorder; Parkinson's disease; episodic paroxysmal anxiety; phobia; migraine; epilepsy; bulimia; stroke cardiovascular disease; heart failure; angina pectoris; obesity; emesis; motility disorder; myocardial infarction; hypertension; dyslipidemia; gastrointestinal disorder; inflammatory bowel disease; osteoporosis; inflammation; infection; pain; cancer; immune disorder; allergy; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                     coupled receptor designated IGS4A. IGS4 exists in two polymorphic forms IGS4A and IGS4B. The IGS4 receptors and IGS4 polynucleotides are useful for preventing, ameliorating or correcting dysfunctions or diseases.
                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gynecological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; G-protein coupled receptor; IGS4; IGS4A; IGS4B; schizophrenia;
                                                                                                              overexpression or
                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents the long version of a human G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SOLV ) SOLVAY PHARM
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DB; AAF80322.
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                                                                              415
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99NL-1013140.
2000EP-0202683.
2000US-0222047.
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99.6%;
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                                                                                                            expression of IGS4.
Score 1252; D
Pred. No. 4.5e
1; Mismatches
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DB 22;
4.5e-141;
hes 0;
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                                      Length
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RESULT 1:
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AC AAB
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24-SEP-1999;
28-JUL-2000;
31-JUL-2000;
          coupled receptor designated IGS4B. IGS4 exists in two polymorphic forms, IGS4B and IGS4B. The IGS4 receptors and IGS4 polynucleotides are useful for preventing, ameliorating or correcting dysfunctions or diseases. These diseases include peripheral nervous system, psychiatric and central nervous system disorders (e.g. schizophrenia, episodic paroxysmal anxiety, phobia, Parkinson's disease, migraine, epilepsy, bulimia or stroke), cardiovascular diseases (e.g. heart failure, angina pectoris, myocardalal infarction or hypertension), dyslipidemias, obesity, emesis, gastrointestinal disorders (e.g. inflammatory bowel disease or motility disorders), osteoporosis, inflammatory importance (e.g. bacterial, fungal, protozoan or viral), pain, cancers, immune disorders, allergies,
                                                                                                                                                                                                                                                                                       New G-protein coupled receptors and the polynucleotides encoding them, useful for preventing, ameliorating or correcting nervous system disorders, cardiovascular diseases, dyslipidemias, inflammations, pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; G-protein coupled receptor; IGS4; IGS4A; IGS4B; schizophrenia; nervous system disorder; psychiatric disorder; parkinson's disease; episodic paroxysmal anxiety; phobia; migraine; epilepsy; bulimia; stroke; cardiovascular disease; heart failure; angina pectoris; obesity; emesis; motility disorder; myocardial infarction; hypertension; dyslipidemia; gastrointestinal disorder; inflammatory bowel disease; osteoporosis; inflammation; infection; pain; cancer; immune disorder; allergy; sepsis;
                                                                                                                                                                                                       The present sequence represents the long version of a human G-protein
                                                                                                                                                                                                                                         Claim 19; Page 85-86;
                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAF80324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gynecological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of a G-protein coupled receptor IGS4B long version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB67804 standard;
                                                                                                                                                                                                                                                                                                                                                                                                           Deleersnijder W,
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gynecological disorders.
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; 2000US-0222047.
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Search completed: January 17, 2003, 05:04:03 Job time: 83 secs

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RESULT T15816

hypothetical protein C48C5.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000

tensin receptor - rat cles: Rattus norvegicus cles: Rattus norvegicus cles: Rattus norvegicus cles: Al-Dec-1991 *sequence considered in the policy	RESULT	. w w w w w w w w a a a a a a
Rattus norvegicus (Norway rat) Rattus norvegicus (Norway rat) -bcc-1991 #sequence_revision 31-bcc-1991 #text_change 17-Mar-2000 -bcc-1991 #sequence_revision of the cloned rat neurotensin receptor tructure and functional expression of the cloned rat neurotensin receptor belongs to the family of G protein-coupled receptor menumber: J70164; MUID:90297956; PMID:1694443 1 424 < TRN> Reurotensin receptor belongs to the family of G protein-coupled receptor modulator in the brain and as a hormone) cellular mediator in peripheral liy: vertebrate rhodopsin G protein-coupled receptor; glycoprotein; transmembrane protein ily: vertebrate rhodopsin G protein-coupled receptor; glycoprotein; transmembrane protein main: transmembrane #status predicted <tm2> Domain: transmembrane #status predicted <tm5> Domain</tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm2>	ALIGNMENTS	31 238.5 18.9 367 2 156520 G protein coupled and 23 238.5 18.9 369 2 529248 somatostatin receptor 32 238.5 18.9 369 2 529248 somatostatin receptor 34 238.5 18.9 370 2 \$43087 orphan opioid receptor 35 238.5 18.9 452 2 \$434916 angiotensin II receptor 36 238.1 8.8 359 2 \$44425 angiotensin II receptor 37 238 18.8 359 2 \$44425 angiotensin II receptor 38 237.5 18.8 359 2 \$4425 angiotensin receptor 41 237 18.8 444 1 \$236.5 angiotensin receptor 42 237 18.8 444 1 \$236.5 \$18.7 387 2 \$15949 galanin receptor 43 236.5 18.7 387 2 \$15949 galanin receptor 44 235 18.6 359 2 \$48857 angiotensin II receptor 44 235 18.6 359 2 \$48857 angiotensin II receptor 45 234 18.5 359 2 \$15194 angiotensin II receptor 46 236.5 18.7 387 2 \$15949 galanin receptor 47 237 18.8 448 1 \$15949 galanin receptor 48 236.5 18.7 387 2 \$15949 galanin receptor 48 256.5 18.7 387 2 \$15949 galanin receptor 48 256.5 18.7 387 2 \$15949 galanin receptor 48 256.5 18.7 387 2 \$15949 galanin receptor 58 25949 galanin receptor 58 25

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-2000
C;Accession: S29506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Cloning and expression of a complementary DNA encoding a high affinity human A; Reference number: S29506; MUID:93154505; PMID:8381365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Vita, N.; Laurent, P.; Lefort, S.; Chalon, FEBS Lett. 317, 139-142, 1993
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A; Introns: 53/3; 87/2; 136/2; 169/3;
C; Superfamily: adenosine receptor Al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C48C5.
A;Reference number: Z18410
A;Accession: T15816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurotensin receptor - human
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A; Residues: 1-378 <FAV>
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R; Favello, A.
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Best Local Similarity
Matches 87; Conserv
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Residues: 1-418 <VIT>
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               112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 VGCYFKTALFETVCFASILSITTVSVERYVAILHP-FRAKLQSTRRRALRILGIVWGFSV 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 VVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 QKHLNSTEEY---LAFLCGPRRSH------
                                                                                                                                                                                                                                             Local
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                                                GTVGNTVTAFTLARKKSLQSLQSTVHYHLGSLALSDLLTLLLAMPVELYNFIWVHHPWAF
                                                                                                                                  DPFQRAQAGLEEALLAPGFGNASGNASERVLAAPSSELDVNTDIYSKVLVTAVYLALFVV 76
                                                                                                                                                                          DPFQKHLNSTEEYL------AFLCGPRRS-----HFFLPVSVVYVPIFVV 55
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      GPVGC---YFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVW 168
                                                                                        GVIGNVLVCLVILQH----QAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYE-MWRNYPFLF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLPMTVISVLYYLMALRVS 241
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                                                                                                                                                                                                                                        Score 325.5;
Pred. No. 1.7
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Pred. No. 3.
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                                                                                                                                                                                                                                           1.7e-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P.; Dumont, X.; Kaghad, M.; Gully,
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A;Cross-references: GB:X97121; NID:g1483579; PIDN:CAA65787.1;
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 20-Jun-2000
C;Accession: 568822
R;Chalon, P; Vita, N.; Kaghad, M.; Guillemot, M.; Bonnin, J.; Delpech, B.;
FEBS Lett. 386, 91-94, 1996
A;Title: Molecular cloning of a levocabastine-sensitive neurotensin binding A;Reference number: S68822; MUID:96228041; PMID:8647296
A;Accession: S68822
A; Molecule type: mRNA
A; Residues: 1-416 < CHA>
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A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Accession: A88013
                                                                                                                                                                                                                   neurotensin receptor 2, levocabastine-sensitive -
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A; Residues: 1-418 <STO>
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FERWLAICHPLRSKIFSTLWRANVLIILAWTISFVCALPIAFIVQINKLPLPEDAKYQPW
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                                                                                                                                                                                                                                                                                                                                                                             ISVLYYLMALRV
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76; Conser
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Pred. No. 1.6e-19;
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                                                                                neurotensin binding site.
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PID:g1483580

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A;Cross-references: GB:M55533
A;Cross-references: GB:M55533
A;Note: the authors translated the codon CTT for residue 213 as Ala, GTG C;Gene: F1yBase:5-HT7
A;Cross-references: F1yBase:FBgn0004573
C;Superfamily: octopamine receptor type I
C;Keywords: G protein-coupled receptor; g1ycoprotein; membrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: hypothalamus C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor; transmembrane pr F;33-58/Domain: transmembrane #status predicted <TM1>F;70-91/Domain: transmembrane #status predicted <TM2>F;110-131/Domain: transmembrane #status predicted <TM3>F;155-175/Domain: transmembrane #status predicted <TM4>F;204-230/Domain: transmembrane #status predicted <TM5>F;296-315/Domain: transmembrane #status predicted <TM6>F;335-361/Domain: transmembrane #status predicted <TM6>F;335-361/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               serotonin receptor 7 - fruit fly (Drosophila melanogaster)
(Alternate names: 5-hydroxytryptamine receptor 7 (5-HTR7)
C;Species: Drosophila melanogaster
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 04-Sep-1998
C;Accession: A38271
R;Witz, P.; Amlatky, N.; Plassat, J.L.; Maroteaux, L.; Borrelli, E.; Hen, R.
Proc. Natl. Acad. Sci. U.S.A. 87, 8940-8944, 1990
A;Title: Cloning and characterization of a Drosophila serotonin receptor tha
;Reference number: A38271; MUID:91062395; PMID:2174167
;Accession: A38271
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TALYSLIFAFGTAGNALSVHVVLKARAGRPGRLRYHVLSLALSALLLLLLVSMPMELYNFV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVVYVPIFVVGVIGNVLVCLVILQHQAMKT-PTNYYLFSLAVSDLLVLLLGMPLEVYE-M 103
CTVCQ---
                                        CTVIKPMWIYNFIIQVTSFL--FYLLPMTVISVLYY
                                                                                   RYLAITKPLEYGVKRTPRRMMLCVGIVWLAAACISLPPLLILGNE-HEDEEGQPI-----
                                                                                                                              RYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPGSAT 200
                                                                                                                                                                                ALSDLCVALLVMPMALLYEVLEKWN-----FGPLLCDIWVSFDVLCCTASILNLCAISVD
                                                                                                                                                                                                          AVSDLLVLLLGMPL----EVYEMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVE 140
                                                                                                                                                                                                                                                                                                                 EEYLA--FLCGPRRSHFFLPVSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFYLLPMTVISVL----YYLMAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRILGIVWGFSVLFSLPNTSIHGIKFHY-FPNGSLVPGSATCTVIKPMWIYNFIIQVTSF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WSHYPWVFGDLGCRGYYF---VRELCAYATVLSVASLSAERCLAVCQPLRARRLLTPRRT 152
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                                                                                                                                                                                                                                                                                                                                                                                      Score 281;
Pred. No. 2
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thyrotropin-releasing hormone receptor - human
(;Specles: Homo sapiens (man)
(;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
(;Accession: $40682; JN0759; $50151; $50152; I38356; JN0708
R;Matre, V.; Karlsen, H.E.; Wright, M.S.; Lundell, I.; Fjeldheim, A.K.; Gabrielsen,
Biochem. Biophys. Res. Commun. 195, 19-185, 1993
A;Title: Molecular cloning of a functional human thyrotropin-releasing hormone recept A;Reference number: $40682; MUID:93371401; PMID:8395824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M59811; GB:M37490; NID:g202153; PIDN:AAA40480.1; C;Superfamily: adenosine receptor Al C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein
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                                                    A;Cross-references: GB:D16845; NID:g577631; PIDN:BAA04120.1; PID:g577632 R;Hinuma, S.; Hosoya, M.; Ogi, K.; Tanaka, H.; Nagai, Y.; Onda, H. Biochim. Biophys. Acta 1219, 251-259, 1994
                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X75071; NID:g404157; PIDN:CAA52965.1; PID:g404158 R;Yamada, M.; Monden, T.; Satch, T.; Satch, N.; Murakami, M.; Iriuchijima, Biochem. Biophys. Res. Commun. 195, 737-745, 193 A;Title: Pituitary adenomas of patients with acromegaly express thyrotropic
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C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 11-Jan-2000
C;Accession: A39251
A; Title: Molecular cloning and functional expression of a A; Reference number: S50151; MUID:95002135; PMID:7918619
                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-398 < MAT>
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A; Residues: 1-398 < YAM>
                                                                                                                                                                                                     A; Reference number: JN0759; MUID: 93384596; PMID: 8396925 A; Accession: JN0759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCLCITYLQYLGINASSCSITAFTIERYIAICHPIKAQFLCTFSRAKKIIIFVWAFTSIY 156
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72; Conserv
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                                                                                                                        A;Cross-references: GB:S60053; NID:g300151; PIDN:AAB26491.1; PID:g300152 C;Superfamily: adenosine receptor A1
                                                                                                                                                                                                                            A; Reference number: A; Accession: I56444
                                                                                                                                                                                                                                        R;Sellar, R.E.; Taylor, P.L.; Lamb, R.F.; Zabavnik, J.; Anderson, L.; Eidne, K.A. J. Mol. Endocrinol. 10, 199-206, 1993
A;Title: Functional expression and molecular characterization of the thyrotrophin-releas A;Reference number: I56444; MUID:93249385; PMID:8387312
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
156444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Вb
                                                                                                                                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                      A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                  A; Residues: 1-411 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:228955; OMIM:188545
A;Map position: 8q23-8q23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Duthie, S.M.; Taylor, P.L.; Anderson, L.; Cook, J.; Ei Mol. Cell. Endocrinol. 95, R11-R15, 1993
A;Title: Cloning and functional characterisation of the A;Reference number: 138356; MUID:94063224; PMID:8243797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-263 <HI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;29-51/Domain: transmembrane *status predicted F;62-83/Domain: transmembrane *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X72089; NID:g440155; PIDN:CAA50979.1; PID:g440156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
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A; Residues: 267-398 <HI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-398 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: I38356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S50152
                                            Matches
                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194-215/Domain: transmembrane
267-288/Domain: transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;146-168/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: adenosine receptor A1
Keywords: G protein-coupled receptor; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene: GDB:TRHR
                                                                                                                                                                                                                                                                                                                                 Accession: I56444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297-319/Domain: transmembrane #status
                                                                                                                                                                                                                                                                                                                           pecies: Mus sp. (mouse)
Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                        rotrophin-releasing hormone receptor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142
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        15
                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .21/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYEMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRR 159
LEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVV----GVIGNVLVCLVILQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSVVYVPIFV-VGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLL-LGMPL---E 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V----FYVVPMILATVLYGFIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IQVTSFLFYLLPMTVISVLYYLMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKKIIIFVWAFTSLYCMLWFFLLDLNISTYKDAIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPGSATC-----TVIKPMWIYNFI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IYGSW-----VYGYVGCLCITYLQYLGINASSCSITAFTIERYIAICHPIKAQFLCTFSR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTILLVLIICGLGIVGNIMVVLVVMRTKHMRTPTNCYLVSLAVADLMVLVAAGLPNITDS 86
                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <NIH>
                                                         20.4%;
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                                            49;
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                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 259;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                            Mismatches
                                                                                                                                                                                                         GB/EMBL/DDBJ
                                                           258;
No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   predicted
                                        DB 2;
1.8e-15;
nes 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <TM5>
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                                        Indels
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                                        36;
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                                   Gaps
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F;32-54/Domain: transmembrane #status predicted <TM2>F;71-92/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                      C; Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                      A;Note: the authors translated the codon ACA for residue 88 as C;Superfamily: adenosine receptor Al
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 30-58,'P',60-222,'T',224
A;Experimental source: strain Wister
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Yamada, M.; Monden, T.; Satoh, T.; IIzuka, M.; Murakami, M.; Iriuchijima, T.; Mori, Biochem. Biophys. Res. Commun. 184, 367-372, 1992
A;Title: Differential regulation of thyrotropin-releasing hormone receptor mRNA level
A;Reference number: PQ0326; MUID:92231953; PMID:1373613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: GH cells
A; Experimental source: GH cells
A; Note: sequence extracted from NCBI backbone (NCBIN:104788, NCBIP:104795)
A; Note: sequence extracted from NCBI backbone (NCBIN:104788, NCBIP:104795)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Molecule type: mRNA
A:Residues: 1-12,'D',14-290,'K',292-412 <ZHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:D17469; NID:g464199; PIDN:BAA04289.1; PID:g464200 R;Chin, W.W.; T R;Zhao, D.; Yang, J.; Jones, K.E.; Gerald, C.; Suzuki, Y.; Hogan, P.G.; Chin, W.W.; T Endocrinology 130, 3529-3536, 1992 A;Title: Molecular cloning of a complementary deoxyribonucleic acid encoding the thyr A;Reference number: A49168; MUID:92283212; PMID:1317787 A;Accession: A49168
                                                                                                                                                                                              F;165-186/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                 F;116-140/Domain:
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A;Title: Cloning and expression of the thyrotropin-releasing A;Reference number: S23436; MUID:92322017; PMID:1377915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status:
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A; Reference number: I53279; MUID:94102223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Kimura, N.; Arai,
Endocrinology 134, 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X64630; NID:g57394; PIDN:CAA45913.1; R;Kimura, N.; Arai, K.; Sahara, Y.; Suzuki, H.; Kimura, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-412 <PEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13
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                                                                                      Matches
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Local Similarity
nes 72; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KHMRTATNCYLVSLAVADLMVLVAAGLPNITDSIYGSW-----VYGYVGCLCITYLQYLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INASSCSITAFTIERYIAICHPIKAQFLCTFSRAKKIIIFVWAFTSIYCMLWFFLLDLNI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QAMKTPTNYYLFSLAVSDLLVLL-LGMPL---EVYEMWRNYPFLFGPVGCYFKTALFETV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-412 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-58,'P',60-222,'T',224-261 <YAM>
                                                                                                                                                                                                                                                                                                            transmembrane #status predicted <TMl>
                                                                                      Conservative
                                                                                                                                                                                                                              transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , K.; Sahara,
432-440, 1994
                                                                                                                   20.4%;
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                                                                                      49;
                                                                                                  Score 258; Db 2,
                                                                                   Mismatches
                                                                                                                                                                                                                           predicted
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                                                                                      ; 08
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                                                                                                                                    Length 412
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                                                                                   36;
                                                                                Gaps
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opioid receptor mu variant MORIA - human
C;Species: Homo sapiens (man)
C;Date: 12-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: $65693; $51216
R;Bare, L.A.; Mansson, E.; Yang, D.
submitted to the EMBL Data Library, July 1994
A;Description: Expression of two variants of the human mu opioid receptor mRNA A;Reference number: $65693
A;Reference number: $65693
A;Rocession: $55693
A;Roceusetype: mRNA
A;Residues: 1-392 <BAR>
A;Cross-references: EMBL:012569; NID:g607911; PIDN:AAB60354.1; PID:g607912
R;Bare, L.A.; Mansson, E; Yang, D.
FEBS Lett. 354, 213-216, 1994
A;Reference number: $51215; MUID:95046336; PMID:7957926
A;Accession: $51215
A;Accession: $51215
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C.Species: Cavia porcellus (guinea pig)
C.Accession: I6595
R; Aharony, D.; Little, J.; Thomas, C.; Powell, S.; Downey-Jones, M.; Graham, J. Recept. Res. 14, 399-421, 1994
A.Title: Isolation and characterization of neurokinin A receptor cDNAs from 6, Reference number: I56595; MUID:95182423; PMID:7877137
A.Accession: I56595
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-402 <RES>
A.; Cross-references: GB:S76253; NID:g913274; PIDN:AAB33553.1; PID:g913275
C.; Superfamily: neurokinin 1 receptor
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C:Species: Cavia porcellus (guinea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMWRNYPFLEGPVGCYEKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRAL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IV----LIYLLPLTVMFVAYSIIGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIW----YFGRAFCYFQNLFPITAMFVSIYSMTAIAIDRYMAIVHPFQPRLSAPSTKA-
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Pred. No. 1.9e-15;
5; Mismatches 71;
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C;Species: Mus musculus (house mouse)
C;Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 24-Nov-1999
C;Accession: A57510; 148665; S66513; 149300
R;Kaufman, D.L.; Keith Jr., D.E.; Anton, B.; Tian, J.; Magendzo, K.; Newman, J. Biol. Chem. 270, 15877-15883, 1995
A;Title: Characterization of the murine mu opioid receptor gene.
A;Reference number: A57510; MUID:95318184; PMID:7797593
                                                                                                                                                                                  A; Residues: 1-398 <ROS>
A; Cross-references: EMBL:U26915; NID:g1055230;
A; Note: the nucleotide sequence was submitted
                                                                               C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G
                                                                                                                                                                                                                                                                                             A; Title: Antisense mapping the MOR-1 opioid receptor: evidence A; Reference number: 149300; MUID:95377399; PMID:7649256 A; Accession: S66513
                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U10561; NID:g555696; PIDN:AAB60673.1; R;Rossi, G.C.; Pan, Y.X.; Brown, G.P.; Pasternak, G.W. FEBS Lett. 369, 192-196, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Min B.H.; Augustin, L.B.; Felsheim, R.F.; Fuchs, J.A.; Loh, Proc. Natl. Acad. Sci. U.S.A. 91, 9081-9085, 1994
A;Title: Genomic structure analysis of promoter sequence of a A;Reference number: I48665; MUID:94377496; PMID:8090773
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                                                                                                                                                                  C; Genetics
                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-398 < RO
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A; Residues: 1-398 < RES>
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                                                                                                                                                 A; Gene: MOR-1
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                   Query Match
Best Local :
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                                                                                                                           95/2; 213/1; 386/3
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                                                                                                                                                                                      EMBL:U26915; NID:g1055230; PIDN:AAA81170.1; PID:g1055231 ide sequence was submitted to the EMBL Data Library, Nove
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                   20.2%;
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28.7%;
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  42;
Score 255; DB Pred. No. 3.1e 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 255.5;
Pred. No. 2.
                                                                               protein-coupled receptor; glycoprotein;
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                 3.1e-J
DB 2; 1
3.1e-15;
nes 84;
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                                     Length 398
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QΥ

34 CGPRR----SHFFLP-----

--VSVVYVPIFVVGVIGNVLVCLVILQHQAMKTP

76

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C:Keywords: G protein-coupled receptor; glycoprotein; F:73-96/Domain: transmembrane #status predicted <TMM1> F:107-132/Domain: transmembrane #status predicted <TMM
                                                                         F;283-304/Domain: transmembrane #status predicted <TMM6>F;323-342/Domain: transmembrane #status predicted <TMM7>F;9,12,33,40,48/Binding site: carbohydrate (Asn) (covale
                                                                                                                                                                        F;107-132/Domain: transmembrane #status predicted <TMM2>
F;144-165/Domain: transmembrane #status predicted <TMM3>
F;188-208/Jomain: transmembrane #status predicted <TMM4>
                                                                                                                                                                                                                                                                                                        A; Map position: 6q24-6q25
C; Superfamily: vertebrate rhodopsin
                                                                                                                                             F;188-208/Domain: transmembrane *status predicted <TMM4> F;236-257/Domain: transmembrane *status predicted <TMM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:L29301; NID:g459831; R;Wang, J.B.; Johnson, P.S.; Persico, A.M.; submitted to GenBank, August 1994 A;Reference number: A38991 A;Accession: A38991 A;Status: translated from GB/EMBL/DDBJ
                                                                                                                              F;283-304/Domain:
                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:137216; OMIM:600018
                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB: OPRM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-50,'N',52-233,'V',235-400 <WAN>
A;Cross-references: GB:L25119; NID:g452072; PIDN:AAA20580.1
R;Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number:
A; Accession: S51215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Expression of two variants of the A; Reference number: S51215; MUID: 95046336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-50,'N',52-400 <WA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S41075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Human mu opiate receptor. cDNA and genomic clones, pharmacologic characterizat A;Reference number: S41075; MUID:94139928; PMID:7905839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-400 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: nucleic acid sequence not shown; translated from GB/EMBL/DDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Title: The human mu opioid receptor: modulation of functional desensitization ;Reference number: I56553; MUID:95198115; PMID:7891175
A;Accession: I56553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Mestek, A.; Hurley, J.H.; Bye, L.S.; Campbell, A.D.; Chen, Y.; Tian, M.; Liu, J. Neurosci. 15, 2396-2406, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: MOR1 protein; opioid receptor mu
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 19-May-2000
C;Accession: I56553; A38991; S41075; S51215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mu opiate receptor - human
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                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bare, L.A.; Mansson, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                 Rtatus: preliminary nolecule type: mRNA Residues: 387-400 <BAR>
  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354, 213-216, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217-222, 1994
  20
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yang, D.
Score
Pred.
253.
                                                                      (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human mu opioid receptor mRNA in SK-N-SH cel PMID:7957926
.5; DB 2
4.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN:AAA20580.1; PID:g452073 Hawkins, A.L.; Griffin, C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN:AAA73958.1; PID:g459832 Hawkins, A.L.; Griffin, C.A.;
                                                                      (covalent) #status
                     2;
                                                                                                                                                                                                                                                                              transmembrane
                       Length 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259
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F;254-281/Domain: transmembrane #status predicted <TMG>
F;288-315/Domain: transmembrane #status predicted <TM7>
F;9,22,29,32,351/Binding site: carbohydrate (Asn) (covalent) #status F;115-193/Disulfide bonds: #status predicted F;250/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kin F;328/Binding site: palmitate (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A41795; MUID:92108031; PMID:1346068
                                       QΥ
                                                                                 Db
                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; P
F;44-69/Domain: transmembrane #status predicted <TM1>
F;80-105/Domain: transmembrane #status predicted <TM2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 17q24-17q24
A; Introns: #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: GDB:SSTR2
A;Cross-references: GDB:134186; OMIM:182452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     somatostatin receptor 2 - human
C; Species: Homo sapiens (man)
C; Date: 31-Dec-1993 #sequence_r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M81830; NID:g307435; PIDN:AAA58248.1; A;Note: sequence extracted from NCBI backbone (NCBIN:74769, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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      142
                                   143 VAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPGSATCT 202
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LAVVHPIKSAKWRRPRTAKMITMAVWGVSLLVILPIMIYAGLRSNQW----
                                                                                                                    LAVSDLLVLLLGMP-LEVYEMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERY
                                                                                                                                                            NQTEPYYDLTSN-----AVLTFIYFVVCIIGLCGNTLVIYVILRYAKMKTITNIYILN 84
                                                                                                                                                                                               NSTEEYLAFICGPRRSHFFLPVSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLE-VYEMWRNYPF 109
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                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                           20.0%;
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                                                                                                                                                                                                                                                                              Score 252.5;
                                                                                                                                                                                                                                                               Pred. No. 4.9e-15;
                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPV
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#status predicted
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ALIGNMENTS

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  Smith R.G., Leonard R., Bailey A.R.T., Palyha O.C., Feighner S.D., Tan C.P., Mckee K.K., Pong S.-S., Griffin P.R., Howard A.D.; "Growth hormone secretagogue receptor family members and ligands." Endocrine 14:9-14(2001).

-!- FUNCTION: Receptor for motilin.

-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE-98110578; pubMed=9441746;
MCKEE K.K., Tan C.P., Palyha O.C., Liu J., Feighner S.D.,
Hreniuk D.L., Smith R.G., Howard A.D., van der Ploeg L.H.T.;
"Cloning and characterization of two human G protein-coupled
genes (GPR38 and GPR39) related to the growth hormone secreta
and neurotensin receptors.";
Genomics 46:426-434(1997).
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Pong S.-S., Austin C.P., Figueroa D., MacNeil D., Cascieri
Nargund R., Bakshi R., Abramovitz M., Stocco R., Kargman S.
O'Neill G., van Der Ploeg L.H.T., Evans J., Patchett A.A.,
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15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Motilin receptor (G protein-coupled receptor)
MTLR1 OR MTLR OR GPR38.
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Mammalia; Eutheria;
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G-protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF034632; AAC26081.1; EMBL; AL137000; CAC19107.1;
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European Bioinformatics Institute.
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CYTOPLASMIC (POTENTIAL)
2 (POTENTIAL)
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Pred.
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-LINKED (GLCNAC. . .) (POTENTIAL).

LVVLAFIICWLPFHVGRIIYINTEDSRMMYESQYFNIVAL
QLFYLSASINPTLYNLISKKYRAAARXLLLARKSRPRGFHR
SRDTAGEVAGDTGGDTVGYTETSANVKTMG -> RKWSRRG
SKDACLQSAPPGTAQTLGPLPLLAQLWAPLPAPFPISIPAS
                                                                                                                                                                                                                                                                                                                              7 (POTENTIAL)
CYTOPLASMIC (
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
                                                                                                                                                                                                                            (IN ISOFORM B).
C13FF6165012DEF3 CRC64;
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4 (POTENTIA)
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3 (POTENTIAL).
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                                                                                                                                                                                    Mismatches
                                                                                                                                                                                             333;
No. 2.
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Query Match

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PRINTS; PR00237; GPCRRHODDPSN.

PRINTS; PR01479; NEUROTENSINR.

PRINTS; PR01480; NEUROTENSNIR.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:97386; Ntsr.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003985; NT1_rec.
InterPro; IPR003984; NT_rec.
                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:97386; Ntsr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as
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Submitted (AUG-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                             G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTSR1 OR NTSR.
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                                                                                                                                                                                                                                                                   Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Snider J., Sano H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fissue-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALCIUM SECOND MESSENGER SYSTEM.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED HIGHEST TO TACHYKININS RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mitted (AUG-1998) to the EMBL/GenBank/DDBJ databases. FUNCTION: RECEPTOR FOR THE TRIDECAPEPTIDE NEUROTENSIN. ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor type 1 (NT-R-1).
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97
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47216
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Rodentia;
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            N-LINKED (GLC)
BY SIMILARITY
PALMITATE (PO)
                                                                                                                                                                                           2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL)

3 (POTENTIAL)
                           N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . . .) (POTENTIAL)
                                                                                                                                            EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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6 (POTENTIAL)
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4 (POTENTIAL).
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                                                                                                                                                                                                                                                                   Palmitate.
ALMITATE (POTENTIAL).
8E9A723171A48711 CRC64;
                                                                                                                                                                                                                                           (POTENTIAL)
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RA DeLoukas P., Matthews L. H., Shurst J., Burton J., Gilbert J.G.R., RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Beasley O.P., Bird C.P., Blakey S.E., Clark L.N., Clark S.Y., Clee C.M., Cley S., Cobbey V.E., Collier R.P., Carder C., Carter N.P., RA Clegg S., Cobbey V.E., Collier R.E., Connor R.E., Corby N.R., RA Clegg S., Cobbey V.E., Collier R.E., Connor R.E., Corby N.R., RA Clegg S., Cobbey V.E., Collier R.E., Connor R.E., Corby N.R., Rall R.E., Rallington A.G., Frankland J.A., Fraser A., French L., Garner P., RA Ellington A.G., Frankland J.A., Fraser A., French L., Howden P.J., Hall R.E., Humt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., RA Huckle E., Hunt A.R., King A., Knights A., Laird G.K., Lawlor S., RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Nickerson T., RA Alley C.M., Sycamore N., Socott C.E., Sehra H.K., Shownkeen R., Sims S., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., RA Swann R.M., Sycamore N., Socott C.E., Sehra H.K., Shownkeen R., Sims S., RA Kay G.C., Lawlin M., Walli M., Walli M., Walli S.M., Thorpe A., RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vita N., Laurent P., Lefort S., Chalon P., Dumont X., Kaghad M Gully D., le Fur G., Ferrara P., Caput D.; "Cloning and expression of a complementary DNA encoding a high affinity human neurotensin receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTSR1 OR NTKK.
HOmo sapiens (Human).
Homosapiens (Chordata; Chorvota; Metazoa; Chordata; Chorvota; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p30989; Q9H4H1; Q9H4H1; 01-JUL-1993 (Rel. 26, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 01-JUL-1993 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) Neurotensin receptor type 1 (NT-R-1) (High-affinity levocabastine-insensitive neurotensin receptor) (NTRH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21638749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93154505; PubMed=8381365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         man neurotensin receptor.";
317:139-142(1993).
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Wray P.W.,

Hubbard T.,

Durbin R.M.,

Bentley D.R., Beck S.,

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PRINTS; PR01480; NEUROTENSNIR.

PROSTTE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSTTE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:8039; NTSR1.
MIM; 162651; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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EMBL; AL357033; CAC14923.1; -.
EMBL; AL355669; CAC12747.1;
PIR; S29506; S29506.
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InterPro; IPR003985; NTI_rec.
InterPro; IPR003984; NT_rec.
Pfam; PF00001; 7tm_1; 2.
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              112
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                                                                                                                                                       Local
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SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
HIGHEST TO TACHYKININS RECEPTORS.
GPVGC---YFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence and core 414:865-871(2001
                                       GTVGNTVTAFTLARKKSLQSLQSTVHYHLGSLALSDLLTLLLAMPVELYNFIWVHHPWAF
                                                               GVIGNVLVCLVILQH---
                                                                                        DPFQRAQAGLEEALLAPGFGNASGNASERVLAAPSSELDVNTDIYSKVLVTAVYLALFVV
                                                                                                                DPFQKHLNSTEEYL------AFLCGPRRS-----HFFLPVSVVYVPIFVV 55
                                                                                                                                                       Similarity
                                                                                                                                                                                            368
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37
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141
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96
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                                                                                                                                                                                             AA;
                                                                                                                                                     25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comparative analysis of
                                                               -QAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYE-MWRNYPFLF 111
                                                                                                                                                                                             MW;
                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC
6 (POTENTIAL
                                                                                                                                                                                                        PALMITATE (POTENTIAL).
T -> A (IN REF. 2).
                                                                                                                                                     Score 325.5;
Pred. No. 9.3
                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                    3 (POTENTIAL)
CYTOPLASMIC (
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2 (POTENTIA:
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5 (POTENTIAL).
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3 (POTENTIAL).
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1 (POTENTIAL).
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                                                                                                                                                                 Length 418;
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Q63384;
01-NOV-1997
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                                                                                                                             PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; DOMAIN 1 32 EXTRACELLULAR
                                                                                                                                                                                                                                                                            EMBL; X97121; CAA65787.1; -. InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was non-profit institutions as long as its content is in no was non-profit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Neurotensin receptor type 2 (NT-R-2) (High-affinity levocabastine-
                TRANSMEM
                                                                                 TRANSMEM
                                                                                                  DOMAIN
                                                                                                               TRANSMEM
                                                                                                                                                                                              PRINTS; PR01481; NEUROTENSN2R
                                                                                                                                                                                                            PRINTS; PR01479; NEUROTENSINR
                                                                                                                                                                                                                               Pfam; PF00001;
                                                                                                                                                                                                                                            InterPro; IPR003986; NT2_rec.
InterPro; IPR003984; NT_rec.
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Delpech B., le Fur G., Ferrara P., Caput D.;
"Molecular cloning of a levocabastine-sensitive neurotensin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sensitive neurotensin receptor).
 DOMAIN
                                 DOMAIN
                                                 TRANSMEM
                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: ABDUNDANT IN CORTEX AND HYPOTHALAMUS, AND LOT
LEVELS SEEN IN THE HEART AND INTESTINE.
DEVELOPMENTAL STAGE: EXPRESSED MAXIMALLY IN 7-DAY-OLD BRAIN AND
EXPRESSION DECREASES PROGRESSIVELY UNTIL ADULTHOOD (35-DAY-OLD
EXPRESSION DECREASES PROGRESSIVELY UNTIL ADULTHOOD (35-DAY-OLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIGHEST TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S Lett. 386:91-94(1996).
FUNCTION: RECEPTOR FOR THE TRIDECAPEPTIDE NEUROTENSIN. IT IS
ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CALCIUM SECOND MESSENGER SYSTEM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLFYLLPMTVISVLYYLMALRVSI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GESVLESLP-----NTSIHGIKEHYEPNGSLV--PGSATCTVIKPMWIYNEIIQVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDAGCRGYYF----LRDACTYATALNVASLSVERYLAICHPFKAKTLMSRSRTKKFISAIW
 33
56
65
88
110
132
155
                                                                                                                                                                                                                               7tm_1;
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d receptor;
32
55
64
87
109
119
1154
176
216
                                                                             1 (POTENTIAL).
CYTOPLASMIC (POTENTE (POTENTE)
               CYTOPLASMIC 4 (POTENTIAL)
                                               EXTRACELLULAR
3 (POTENTIAL).
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                              (POTENTIAL).
                                                                                                (POTENTIAL).
                                                                                                                             Lipoprotein; Palmitate. (POTENTIAL).
(POTENTIAL)
                                                                (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND LOWER
                                                                                                                                                                                                                                                                                                                                                                                                                          collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218
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RESULT 6
5HT1_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFT
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferriera S., Fleischmann W.,
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p20905; Q9VA21;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5-hydroxytryptamine receptor 1 (5-HT receptor
5-HT7 OR 5HT-R1 OR CG12073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DISULFID
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DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brack Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                Witz P., Amlaiky N., Plassat J.-L., Maroteaux L., Borrelli E., Hen R.; "Cloning and characterization of a Drosophila serotonin receptor that activates adenylate cyclase."; Proc. Natl. Acad. Sci. U.S.A. 87:8940-8944(1990).
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91062395; PubMed=2174167;
Witz P., Amlaiky N., Plassat J.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Oregon-R; TISSUE=Head;
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                                                                                                                                                                                                                                                                                   MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WRNYPFLFGPVGC---YFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVVYVPIFVVGVIGNVLVCLVILQHQAMKT-PTNYYLFSLAVSDLLVLLLGMPLEVYE-M 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
PALMITATE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127FC5F5CB6FE208 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281;
No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor) (Serotonin receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95
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Query Match Best Local

Similarity

22.2%;

Score 281; Pred. No. 1

DB 1; .9e-1

Length 564;

Indels

28;

Gaps

9

ÃĄ,

MM

0C8B9F8DA63D8095

Conservative

36;

Mismatches

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RA Harris N.L., Harvey D., Heiman T.J., Wein, Gudir F., Hallis M.,

RA HOSTIN D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kinmel B.E., Kodira C.D., Kraft C.K., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Raizzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Raizzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Raizzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Spier E., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Wang A.H., Wang X.,

RA Wang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Wang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Wang Z.-Y. Wassarman D.A., Wolley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

"The genome sequence of Drosophila melanogaster.";

"The Stence 287:2185(2000).

CC 5-HYDROXYRYPTAMINE (SEROTONIN), A BIGGENIC HORMONE THAT FUNCTIONS

AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF

THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE
 DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_l, 1.

PRINTS; PR00237; GPCRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                      G-protein TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0004573; 5-HT7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A38271; A3827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE003776; AAF57104.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M55533; AAA28305.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                          TRANSMEM
                                                                                           DOMAIN
                                                                                                               TRANSMEM
                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                    TRANSMEM
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                                                                                                                                                    FRANSMEM
                                                                                                                                                                     DOMAIN
                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: HEAD.
SIMILARITY: BELONGS TO FAMILY 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein. TISSUE SPECIFICITY: HEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BUT WITH ONE EXTRA POTENTIAL TRANSMEMBRANE DOMAIN.
                                                                                                                                                                                                                                                                                                                                     coupled
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                                                                                                                                                                                                                                                                                                                                       receptor;
106
314
60861
                                                      198
222
236
258
258
278
278
302
330
353
454
476
487
564
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                                                                        EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                  Transmembrane;
0 (POTENTIAL)
                   Вү
                                 CYTOPLASMIC (POTENTIAL).

9 X 2 AA TANDEM REPEATS OF
                                                                                                                                                                                                                                                             CYTOPLASMIC
2 (POTENTIA)
                                                                                                                                                                                       CYTOPLASMIC
4 (POTENTIA
                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL) 3 (POTENTIAL).
                                                                                                                                                                                       (POTENTIAL)
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                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                   SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no rest
                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Repeat
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B)
MEDLINE=21255649; PubMed=11356716;
Petersenn S., Rasch A.C., Penshorn M.,
"Genomic structure and transcriptional
hormone secretagogue receptor.";
Endocrinology 142:2649-2659(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHSR_HUMAN STANDARD; PRT; JDD AA. (292847; Q92848; Q95RJ7; 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Growth hormone secretagogue receptor type 1 (peptide receptor) (GHRP) (Ghrelin receptor).
                                                                                                                                                          MEDLINE=20067959; PubMed=10604470;
Kojima M., Hosoda H., Date Y., Nakazato
"Ghrelin is a growth-hormone-releasing a
                                                                                                                                                                                                                                                                                         Smith
Tan C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Howard A.D., Feighner S.D., Cully D.F., Arena J.P.,
Liberator P.A., Rosenblum C.I., Hamelin M., Hreniuk D.L.,
Palyha O.C., Anderson J., Paress P.S., Dlaz C., Chou M., Liu K.K.,
McKee K.K., Pong S.-S., Chaung L.-Y., Elbrecht A., Dashkevicz M.,
Heavens R., Rigby M., Sirinathsinghji D.J.S., Dean D.C., Melillo D.
Patchett A.A., Nargund R., Griffin P.R., Demartino J.A., Gupta S.K.
Schaeffer J.M., Smith R.G., van der Ploeg L.H.T.;
"A receptor in pituitary and hypothalamus that functions in growth
                                                                                                                                                   stomach.
                                                                                                                                                                                                                      FUNCTION
                                                                                                                                                                                                                                                                Smith R.G., Leonard R., Bailey A.R.T., Palyha O.C., Feighner S.D., Tan C.P., McKee K.K., Pong S.-S., Griffin P.R., Howard A.D.; "Growth hormone secretagogue receptor family members and ligands.";
                                                                                                                                                                                                                                                                                                                        MEDLINE=21219832; PubMed=11322507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hormone release.";
Science 273:974-977(1996).
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MEDLINE=96337998; PubMed=8688086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314
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as well as non-peptide, low molecular weight sec
L-692,429, MK-0677, adenosine).
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1A (SHOWN HERR
                                                    FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 prote Stimulates growth hormone secretion. Binds also other growth hormone releasing peptides (GHRP) (e.g. Met-enkephalin and as well as non-peptide, low molecular weight secretagogues
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                                                                                                                             402:656-660(1999).
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       HERE) AND
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growth
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Gupta S.K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TISSUE SPECIFICITY:
SIMILARITY: BELONGS
                                                                          QYRPWNFGDLLCKLFQFVSESCTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVI
                                                                                                                   VTATCVALFVVGIAGNILTMLVVSRFRELRTTTNLYLSSMAFSDLLIFLC-MPLDLVRLW
                                                                                                                                      VSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMW
                  IIQVTSFLFYLLPMTVISVLYYLMALRV
                                   FVIWAVAFCSAGPIFVLVGVEHE---NGTDPWDTNECRPTEFAVRSGLLTVM--VWV---
                                                         GIVWGFSVLFSLPNTSIHGIKFHYFPNGS----
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-SSIFFFLPVFCLTVLYSLIGRKL
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TO FAMILY 1 OF G-PROTEIN CO
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CYTOPLASMIC (POTENTIAL)
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Pred. No. 2.
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7; Mismatches
                                                                                                                                                                                                             AVVVFAFILCWLPFHVGRYLFSKS -> PILSLCLLPSL (IN ISOFORM 1B). MISSING (IN ISOFORM 1B).
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CYTOPLASMIC (
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008725;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Growth hormone secretagogue receptor type 1 (
                                                                                                                                TRANSMEM
DOMAIN
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PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                G-protein
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KOjima M., Hosoda H., Date Y., Nakazato M., Matsuo H.,
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Takahara J.;
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MEDLINE=97246555; PubMed=9092793;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hormone releasing peptides (GHRP) (e.g. Met-enkephalin and as well as non-peptide, low molecular weight secretagogues L-692,429, MK-0677, adenosine) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins. Stimulates growth hormone secretion. Binds also other growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through meen the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content by non-profit institutions as l
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      411
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73
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118
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184
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236
286
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                                                                                                                                                                                                                                                                                                                                                                                                        BAA21777.1; ALT_INIT
                                                                                                                                                                                                                                                                                receptor;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsubara
4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                  Transmembrane; Glycoprotein.
EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
                                                                                                                              EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                           CYTOPLASMIC
2 (POTENTIAL
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Sciurognathi;
                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohye H., Niimi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata;
thi; Muridae;
                                                                                                                                                                                                               (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GHS-R)
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; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GH-releasing
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                                                                                                                                                                                                                                                                                                                              STRAIN-Yorkshire; TISSUE-Pituitary;

X MEDLINE-96337998; pubMed-8688086;

X MEDLINE-96337998; pubMed-8688086;

X MEDLINE-96337998; pubMed-8688086;

X MEDLINE-96337998; pubMed-8688086;

X Medition S.D., Cully D.F., Arena J.P.,

X Liberator P.A., Rosenblum C.I., Hamelin M., Hreniuk D.L.,

X Palyha O.C., Anderson J., Paress P.S., Diaz C., Chou M., Liu K.K.,

X Palyha O.C., Anderson J., Paress P.S., Diaz C., Chou M., Liu K.K.,

X Palyha O.C., Anderson J., Paress P.S., Diaz C., Chou M., Liu K.K.,

X Palyha O.C., Anderson J., Paress P.S., Diaz C., Chou M., Liu K.K.,

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X Palyha O.C., Anderson J., Paress P.S., Diaz C., Chou M., Liu K.K.,

X Heavens R., Rigby M., Sirinathsinghji D.J.S., Dean D.C., Melillo D.G.,

X Heavens R., Rigby M., Sirinathsinghji D.J.S., Dean D.C., Melillo D.G.,

X Heavens R., Rigby M., Sirinathsinghji D.J.S., Dean D.C., Melillo D.G.,

X Heavens R., Rigby M., Sirinathsinghji D.J.S., Dean D.C., Melillo D.G.,

X Heavens R., Rigby M., Sirinathsinghji D.J.S., Dean D.C., Melillo D.G.,

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X Heavens R., Rigby M., Sirinathsinghji D.J.S., Dan D.C., Melillo D.G.,

X Heavens R., Rigby M., Sirinathsinghji D.J.S., Dan D.C., Melillo D.G.,

X Heavens R., Rigby M., Sirinathsinghji D.J.S., Diaz C., Chou M., Liu K.K.,

X Heavens R., Rigby M., S
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Matches 66
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CARBOHYD
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  use by modified
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                       the
                                                                                                                                                             SECRETAGOGUES.
-!- TISSUE SPECIFICITY:
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHSR
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                    ween the Swiss Institute of Bioinform
European Bioinformatics Institute. The
by non-profit institutions as long
                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1A (SHOWN HERI PRODUCED BY ALTERNATIVE SPLICING. ISOFORM 1B API
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSVVYVPIEVVGVIGNVLVCLVILQHQAMKTPTNYYLESLAVSDLLVLLLGMPLEVYEMW
                                                                                                            SWISS-PROT entry is copyright.
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Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40963
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31.7%;
                                                                                                                                                                   PITUITARY
TO FAMILY
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BY SIMILARITY
N-LINKED (GLCNAC. ...
N-LINKED (GLCNAC. ...
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                                                                      Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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No. (
     removed.
                                                                                                         It is produced through a collaboration
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                                                                                                                                                                                                HYPOTHALAMUS
                                                                                                                                                                   G-PROTEIN COUPLED RECEPTORS
                       There are no rest
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د.
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TRFR_CHICK
ID TRFR_C
AC 093603
DT 30-MAY
DT 30-MAY
DT Trecept
DE Thyrot
DE recept
OS Gallus
OC Archos
OC Archos
OC ARCBL_T
RN [1]
RP SEQUEN
RC TISSUE
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Best Local S
Matches 66
                                                                                                           093603;
30-MAY-2000
30-MAY-2000
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
SEQUENCE
  TISSUE-Pituitary;
                                                                                               Thyrotropin-releasing
                                                      Archosauria; Aves;
                                                                 Eukaryota; Metazoa;
                                                                                       receptor)
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#fam; PF00001; 7tm_1; 1.

#RINTS; PR00237; GPCRRHODOPSN.

#PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

##ROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

##ROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

##ROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                               NCBI_TaxID=9031;
                                                                                                                                                       TRFR_CHICK
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                                                                                                                                                                                                             217
                                                                                                                                                                                                                              213 IIQVTSFLFYLLPMTVISVLYYLMALRV 240
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                                                                                                                                                                                                                                                                      GIVWGFSVLFSLPNTSIHGIKFHYFPNGS------LVPGSATCTVIKPMWIYNF
                                                                                                                                                                                                                                                                                             QYRPWNLGNLLCKLFQFVSESCTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVI
                                                                                                                                                                                                                                                                                                          ----SSVFFFLPVFCLTVLYSLIGRKL 239
                                                                                                                                                                                                                                                   LVIWAVAFCSAGPIFVLVGVE---HDNGTDPRDTNECRATEFAVRSGLLTVM--VWV---
                                                                                                                                                                                                                                                                                                                                       VTATCVALFVVGIAGNLLTMLVVSRFREMRTTTNLYLSSMAFSDLLIFLC-MPLDLFRLW
                                                                          gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                     66;
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             290
366 AA;
                                                                                            (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
-releasing hormone receptor (TRH-R)
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                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                     STANDARD;
                                                      Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                              366
41194
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
Weognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                    47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 4.207; Mismatches
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2 (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                            Score 274;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
AVVYFAFILCWLPFHVGRYLFSKS -> GGSQCAL
PLHSSCLFSSP (IN ISOFORM 1B).
MISSING (IN ISOFORM 1B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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7 (POTENTIAL).
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5 (POTENTIAL).
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                                                                                                                                                     395
                                                                                                                                                    ΑA
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                                                                                               (Thyroliberin
                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                    Phasianinae;
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sequence update) annotation updat

update)

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GHSR_MOUSE
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Best Local S
Matches 72
  GHSR_MOUSE STAN
Q99P50; Q91Z82;
15-JUN-2002 (Rel. 4
15-JUN-2002 (Rel. 4
15-JUN-2002 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Endocrinology 139:3390-3398(1998).
Endocrinology Endocrinology 139:3390-3398(1998).
FUNCTION: RECEPTOR FOR THYROTROPIN-RELEASING HORMONE.
RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A
PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                       62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QNHTGLLLSSQEFVT-----AEYQVVTILLVLLICGLGIVGNIMVVLVVLRTKHMRTP
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1 30
4 31 53
54 63
M 64 85
M 102 123
M 124 146
M 124 146
M 195 217
171 195
EM 269 290
EM 269 321
EM 299 321
SEM 299 321
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                                                                                                  STANDARD;
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Last sequences Last anno
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CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane: Glycoprotein EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 8e-
2; Mismatches
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CYTOPLASMIC (
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7 (POTENTIAL).
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4 (POTENTIA)
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of the chicken thyrotropin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291D9BD2718723CB CRC64;
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                                                                                               257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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(GHS-R) (GH-releasing

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                                                                                                                                               RT RAP
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                                                                                              Matches
                                                                                                          Query Match
Best Local
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EMBL; AF332997; AAG61141.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peng X., Frohman L.A., Kinem Submitted (JAN-2001) to the
                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                        G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=129S3/SvImJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning of mouse ghrelin/growth hormone secretagogue receptor cDNA rapid amplification of cDNA ends (RACE).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               orowin normone secretagogue receptor type 1 (GHS-R) (Ghipeptide receptor) (GHRP) (Ghrelin receptor) (Fragment). GHSR.
                                                                                                                                                          NON
                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                 TRANSMEM
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                                                                                                                                                                                                                                                                                                                                TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota;
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
 104
                         105
                                                45
                                                                        45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins. Stimulates growth hormone secretion. Binds also other growth hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6) as well as non-peptide, low molecular weight secretagogues (e.g. L-992,429, MK-0677, adenosine) (By similarity). SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute.
QYRPWNFGDLLCKLFQFVSESCTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVI
                     RNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRIL 164
                                                           VSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMW 104
                                             VTATCVALFVVGISSNLLTMLVVSRFRELRTTTNLYLSSMAFSDLLIFLC-MPLDLVRLW 103
                                                                                                                                                                                                                                                                                                                                                                                                       PF00001;
                                                                                              65;
                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                 PS00237; G_PROTEIN_RECEP_F1_1; PS50262; G_PROTEIN_RECEP_F1_2;
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                                                                                                                                                                                                                                                                                                                                                        coupled
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lus (Mouse)
Metazoa; (
                                                                                                                                 101 125
126 148
149 160
61 183
34 211
2 257
197
13
26
187
28743 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-183 FROM N.A.
L/6J; TISSUE=Hypothalamus;
                                                                                                                                                                                                         36
59
78
101
126
126
149
161
184
212
235
                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       7tm_1;
                                                                                                                                                                                                                                                                                                                                                       receptor;
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Rodentia;
                                                                                                          21.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kineman R.D.;
                                                                                              47;
                                                                                                                                                                                                                                                                                                     1 (POTENTIAL).
CYTOPLASMIC (PO
                                                                                                                                                                                                                                                                                                                                         Transmembrane; Glycoprotein.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases
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                                                                                                       Score
Pred.
                                                                                                                                                                                            BY SIMILA
                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL) 5 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                     N-LINKED
                                                                                                                                                                                  N-LINKED
                                                                                                                                                                                                                                                                    CYTOPLASMIC
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3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                             D6FA21EAB0E30791
                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                              Mismatches
                                                                                                                                                                                                        SIMILARITY
                                                                                                         268;
10. 8.
                                                                                                                                                                  (GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions
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                                                                                                                                                                                                                                                                   (POTENTIAL)
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                                                                                                                    1;
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                                                                                             70;
                                                                                                                                             CRC64;
                                                                                                                   Length 257;
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL
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TRFR_MOUSE
                                                                                                                                        EMBL; M59811; AAA40480.1; -.
EMBL; M94384; AAA40437.1; -.
EMBL; L48936; AAA81559.1; -.
PIR; A39251; A39251.
                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                          Jones K.E., Brubaker J.H., Chin W.W.; "An alternative splice variant of the mouse TRH receptor mRNA is the major form expressed in the mouse pituitary gland."; J. Mol. Endocrinol. 16:197-204(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Straub R.E., Frech G.C., Joho R.H., Gershengorn M. "Expression cloning of a cDNA encoding the mouse p thyrotropin-releasing hormone receptor.";
Proc. Natl. Acad. Sci. U.S.A. 87:9514-9518(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last seq
01-NOV-1997 (Rel. 35, Last ann
                          PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein.

DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
                                                                                                                           MGD;
                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Narayanan C.S., Fujimoto J., Geras-Raaka E., Gershengorn M.C. "Regulation by thyrotropin releasing hormone (TRH) of TRH remarka degradation in rat pituitary GH3 cells."; J. Biol. Chem. 267:17296-17303(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Pituitary;
MEDLINE=91088548; PubMed=2175902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thyrotropin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P21761;
01-MAY-1991
 DOMAIN
                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97013702; PubMed=9156522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 332-393 FROM N.A.
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                                                                                           InterPro; IPR000276; GPCR_Rhodpsn
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: RECEPTOR FOR THYROTROPIN-RELEASING HORMONE. RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A
                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                           MGI:98824; Trhr.
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1 receptor;
28
51
61
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Rodentia;
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Last annotation 
hormone receptor
 CYTOPLASMIC
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 (POTENTIAL)
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RESULT 13
TRFR_HUMAN
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Best Local :
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=93371401; PubMed=8395824;
Matre V., Karlsen H.E., Wright M.S., Lund,
Matre V., Karlsen H.E., Gautvik K.

"'''s functional human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
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TRANSMEM
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TRANSMEM
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TRANSMEM
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TRANSMEM
expression gene.";
       "Pituitary adenomas of patients with acromegaly express thyrotropin-releasing hormone receptor messenger RNA: cloning and functional expression of the human thyrotropin-releasing hormone receptor
                                                          TISSUE=Pituitary; MEDLINE=93384596;
                                                                                                    Biochem.
                                                                                                                                                                                     'GCepro
TRHR.
Homo sapiens (Human).
Homo sapiens (Human).
Theria; Primates;
                                                                                                                                                                                                                                               Thyrotropin-releasing
                                                                                                                                                                                                                                                                            P34981;
01-FEB-1994
                                                                                                                                                                                                                                                                                                  TRFR_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                       Kakegawa
                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                      receptor).
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                                      Yamada M., Monden
Kakegawa T., Mori
                                                                                                              hormone receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNVLVCLVIIQHQAMKTPTNYYLFSLAVSDLLVLL-LGMPL---EVYEMWRNYPFLFGPV
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                                       Mori M.;
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                                               PubMed=8396925;
T., Satoh T., Satoh N.,
                                                                                                    Res.
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Last annotation update)
hormone receptor (TRH-R
                                                                                                                                                                                                                                                                             Created)
                                                                                                   Commun.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL N-LINKED (GLCNAC. . .) N-LINKED (GLCNAC. . .) ; 8739B75D1A0FCCFC CRC
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5 (POTENTIAL).
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4 (POTENTIA)
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3 (POTENTIAL).
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Catarrhini;
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ik K.M.;
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                                                Murakami M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
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                                                 Iriuchijima
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EMBL; D16845; BAA04120.1;
EMBL; X75071; CAA55965.1;
EMBL; X75078; CAA50979.1;
EMBL; S75283; AAB32222.1;
EMBL; S75281; AAB32222.1;
EMBL; S75281; AAB32222.1;
EMBL; D85376; BAA12796.1;
EMBL; D85376; BAA12796.1;
EMBL; D85375; BAA12796.1;
EMBL; D85375; CAA09746.1;
                        TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human thyrotropin-releasing hormone receptor.";
J. Neurochem. 72:40-50(1999)
-i- FUNCTION: RECEPTOR FOR THYROTROPIN-RELEASING HORMONE.
RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A
PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                                                                           PIR;
PIR;
                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hinuma S., Hosoya M., Ogi K., Tanaka H., Naga "Molecular cloning and functional expression releasing hormone (TRH) receptor gene." Biochim. Biophys. Acta 1219:251-259(1994).
                                                                                                             G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matre V., Hovring P.I., Velickovic Z., Murray-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Placenta;
MEDLINE=99101143;
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"Genomic organization and promoter function releasing hormone receptor gene.";
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                                                                                     TRANSMEM
                                                                                                                                                              InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                        MIM; 188545;
                                                                                                                                                                                                  Genew; HGNC:12299;
                                                                                                                                                                                                                PIR;
                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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S40682; S40682.
JN0708; JN0708.
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                                                                                                            PS00237; G_PROTEIN_RECEP_F1_1; 1. PS50262; G_PROTEIN_RECEP_F1_2; 1. n coupled receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .M., Taylor P.L., Anderson L., Cook J.,
and functional characterisation of the
1. Endocrinol. 95:R11-R15(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF 1-263 FROM N.A.
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receptor;
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           EXTRACELLULAR (
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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2 (POTENTIA)
                                                                                   EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL)
 EXTRACELLULAR (POTENTIAL)
                                                             (POTENTIAL)
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Best Local
                                                                                                                                                                                 "Molecular cloning o. gene.";
J. Vet. Med. Sci. 60.
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046639;
16-OCT-2001
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16-OCT-2001
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CARBOHYD
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TRANSMEM
                                                     use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                               This
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                               BOVIN
                       EMBL; D83964;
                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                          MEDLINE-98151337; PubMed-9492373;
                                                                                                                                                                                                                                                         STRAIN-Holstein;
                                                                                                                                                                                                                                                                                                                                        Bos taurus
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                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                              receptor).
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                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                         FUNCTION: RECEPTOR FOR THYROTROPIN-RELEASING HORMONE. RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A RECEPTOR IS MEDIATED ACCIUM SECOND MESSENGER SYSTEM.
                                                                                      SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN 
Buropean Bioinformatics Institute. There are no rest
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          IPR000276;
                                           email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       (Bovine).
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
-releasing hormone receptor (TRH-R) (Thyroliberin
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                     BAA24069.1;
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RECEPTOR FOR THYROTROPIN-RELEASING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                     Y., Ikeda
of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215
266
288
296
319
398
398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45084
         GPCR_Rhodpsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-> K (IN DBSNP:5774).

/FTId=VAR_011857.

W; FE920B5F2E933D3E CRC64;
                                                                                                                                                                                                                 A., Sekikawa K.;
thyrotropin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 (POTENTIAL).
CYTOPLASMIC (P
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL) 7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259;
No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                  398
                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
3.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ĄĄ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                             as its content
                                                                Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 398;
                                                                                                                                                                                                                                                                                                             Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                     hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                 у
                                                                                        restrictions
                                                                  and
                                                                                                  EMBL outstation
                                                                             ıs
                                                                                                               b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
                                                                  for
                                                                                                    collaboration - 
L outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                 commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                             no
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20
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                                                                                                                                                                                                                                                                                                                                                                    D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                              Q28596;
01-NOV-1997
01-NOV-1997
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
  + +
                                                                                                                     TISSUE=Pituitary;
MEDLINE=97200775; PubMed=9048604;
                                                                                                                                                                                                                                                                                                                        _SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-protein
DOMAIN
                     ENDOCTIONLOGY 138:1019-1028(1997).

11- FUNCTION: RECEPTOR FOR THYROTROPIN-RELEASING HORMONE.

RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A
PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                    Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00237; PROSITE; PS50262;
                                                                  "Thyrotropin expression in is 3,5,3'-triiodothyronine, independent.";
                                                                                                  Bockmann J., Boeckers T
Deufel T., Kreutz M.R.;
                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                       Eukaryota;
                                                                                                                                                                                                                 Ovis aries
                                                                                                                                                                                                                               TRHR
                                                                                                                                                                                                                                        receptor).
                                                                                                                                                                                                                                                  Thyrotropin-releasing
                                                                                                                                                                                                                                                                                                           TRFR_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                    198
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                                                                                                                                                                                                                                                                                                                                                                                          214
                                                                                                                                                                                                                                                                                                                                                                                                                142
                                                                                                                                                                                                                                                                                                                                                                                                                                       160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27
 SUBCELLULAR SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSVYYVPIFV-VGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLL-LGMPL---E
                                                                                                                                                                                                                                                                                                                                                                      V-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYEMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRR 159
                                                                                                                                                                                                                                                                                                                                                                                                               AKKIIIFVWAFTSIYCMLWFFLLDLNISTYKDAIVV----SCGYKISRNYYSPIYLMDFG
                                                                                                                                                                                                                                                                                                                                                                                                                                     ALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPGSATC-----TVIKPMWIYNFI 213
                                                                                                                                                                                                                                                                                                                                                                                      IQVTSFLFYLLPMTVISVLYYLMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            IYGSW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTILLVLIICGLGIVGNIMVVLVVMRTKHMRTPTNCYLVSLAVADLMVLVAAGLPNITDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coupled
                                                                                                                                                                                                      (Sheep).
Metazoa;
                                                                                                                                                                                                                                                            (Rel. 35, (Rel. 36,
                                                                                                                                                                                                                                                                                                                                                                  -FYVVPMILATVLYGFIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                    (Rel.
                                                                                                             Boeckers T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -VYGYVGCLCITYLQYLGINASSCSITAFTIERYIAICHPIKAQFLCTFSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                            STANDARD;
LOCATION: Integral membrane protein. BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor; 2
28
51
61
83
99
1121
1144
1168
1193
215
215
286
286
286
286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G_PROTEIN_RECEP_F1_1;
                                                                                                                                                                                                                                                                                    35,
                                                                                                                                                                                         Chordata; Craniata; Vertebra
Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.4%;
                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                  hormone receptor (TRH-R) (Thyroliberin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
                                                                            hypophyseal pars tuberalis-specific , thyrotropin-releasing hormone, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Glycoprotein.
EXTRACELLULAR (POTENTIAL).
                                                                                                               Winter C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 258; Db 1,
No. 6.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL)

7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                                    215
                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D9AF4B211A5701B8 CRC64;
                                                                                                                                                                                                                                                                                                           398
                                                                                                             Wittkowski W.,
                                                                                                                                                                                                      Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 398;
                                                                                                                                                                                              Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                               Winterhoff H.,
                                                                                                                                                                                             Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                              cells
pit-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
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QΥ
                                                        뫄
                                                                               QΥ
                                                                                                             В
                                                                                                                                     Qγ
                                                                                                                                                                  DЪ
                                                                                                                                                                                       ρy
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                            TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G_Protein coupled receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X95285; CAA64606.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00001; 7tm_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                        142
                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
198 V-----FYVVPMILATVLYGFIA 215
                                                                                                                       100 VYEMWRNYPELFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPERAKLQSTRRR 159
                           214 IQVTSFLFYLLPMTVISVLYYLMA 237
                                                                         160 ALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPGSATC----TVIKPMWIYNFI 213
                                                                                                                                                                             87 IYGSW-----VYGYVGCLCITYLQYLGINASSCSITAFTIERYIAICHPIKAQFLCTFSR 141
                                                                                                                                                                  27
                                                 AKKIIIFVWAFTSIYCMLWFFLLDLNISTYKDAIVV----SCGYKISRNYYSPIYLMDFG 197
                                                                                                                                                            VTILLVLIICGLGIVGNIMVVLVVMRTKHMRTPTNCYLVSLAVADLMVLVAAGLPNITDS 86
                                                                                                                                                                                                                                                                         398 AA;
                                                                                                                                                                                                                   Conservative 47; Mismatches
                                                                                                                                                                                                                                                                                                                29
52
52
62
100
122
145
145
2164
2267
287
287
                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                           45088 MW;
                                                                                                                                                                                                                               20.4%; Score 258; DB 1; Length 398; 32.4%; Pred. No. 6.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Glycoprotein.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                      5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL)
                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

; 375A311D3DD2A61A CRC64;
                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL) 5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                            4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                       3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                  Indels 26;
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                  7;
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Earch completed: January 17, 2003, 05:04:48 ob time : 35 secs

5.1.3

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ring table:
    January 17, 2003, 05:04:56; Search time 64 Seconds (without alignments) 75.166 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-684-725-2
1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120991 segs, 19878514 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
: /cgn2_6/ptodata/2/pubpaa/US07_FUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_FUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_NEW_FUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_FUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US10_NEW_FUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US10_NEW_FUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US10_NEW_FUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEKLQNASWIYQQKLEDPFQ.....LLPMTVISVLYYLMALRVSI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                           /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

19	18	17	16	15	14	13	12	11	10	9	æ	7	ത	U	4	ω	2		No.
200) N	255	255	255	255	255	255	255	255	255	256.5	262.5	262.5	262.5	262.5		262.5	418	Score
20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2		20.3		20.8				20.8	33.1	Match Length
444	438	409	401	398	398	398	398	392	391	390	415	259	259	259	259	259	222	419	
T	10	10	10	12	10	10	10	10	10	10	10	10	9	9	9	9	10	10	₽B
US-U9-761-962-28	US-09-761-962-17	-761-96	US-09-761-962-20	US-10-039-645-83	US-09-966-871-83	US-09-761-962-29	US-09-214-904-2	US-09-761-962-19	6	US-09-761-962-25	US-09-823-114-20	US-09-796-338A-23	US-10-077-698-3	US-10-012-140-29	US-10-012-140-27	US-10-080-960-25	US-09-911-005-4	US-09-804-551B-26	ID
Sequence 28, Appl	Sequence 17, Appl	Sequence 27, Appl	Sequence 20, Appl	Sequence 83, Appl	Sequence 83, Appl	Sequence 29, Appl	Sequence 2, Appli	Sequence 19, Appl	Sequence 26, Appl	Sequence 25, Appl	20,	ω	Sequence 3, Appli	Sequence 29, Appl	Sequence 27, Appl	Sequence 25, Appl	Sequence 4, Appli	Sequence 26, Appl	Description

RESULT 2

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	
234.5	237	238.5	239	239	240.5	240.5	242	242	242.5	242.5	242.5	242.5	242.5	244.5	246.5	246.5	247.5	251.5	251.5	253	253	253.5	253.5	254.5	
18.6	18.8	18.9	18.9	18.9	19.0	19.0	19.2	19.2	19.2	19.2	19.2	19.2	19.2	19.4	19.5	19.5	19.6	19.9	19.9	20.0	20.0	20.1	20.1	20.2	
453	460	370	359	359	398	398	359	359	398	398	398	382	367	506	400	400	369	400	400	383	383	400	400	405	
9	9	10	10	9	12	10	12	10	12	10	10	10	10	10	12	10	10	12	10	12	10	12	10	12	
US-09-970-966-209	US-10-166-101-4	US-09-823-114-19	US-09-867-569-9	US-09-867-915-3	US-10-039-645-79	US-09-966-871-79	US-10-039-645-81	US-09-966-871-81	US-10-039-645-1	US-09-966-871-1	US-09-823-114-16	US-09-993-844-4	US-09-823-114-23	US-09-804-551B-34	US-10-039-645-78	US-09-966-871-78	US-09-823-114-9	US-10-039-645-86	US-09-966-871-86	US-10-039-645-87	US-09-966-871-87	US-10-039-645-85	US-09-966-871-85	-645	
Sequence 209, App	Sequence 4, Appli	Sequence 19, Appl	Sequence 9, Appli	Sequence 3, Appli	Sequence 79, Appl	Sequence 79, Appl	Sequence 81, Appl	Sequence 81, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 16, Appl		23	34,	Sequence 78, Appl	Sequence 78, Appl	Sequence 9, Appli	Sequence 86, Appl	Sequence 86, Appl	Sequence 87, Appl	Sequence 87, Appl	Sequence 85, Appl	Sequence 85, Appl	•	

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US-09-804-551B-26
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Patent No. US2002056151A1
GENERAL INFORMATION:
APPLICANT: Bayer Aktiengesellschaft
TITLE OF INVENTION: Receptors for peptides from insects
FILE REFERENCE: Le A 34 394
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. SEQ ID NO 26
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/804,551B CURRENT FILING DATE: 2001-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: DE 100 13 618.4 PRIOR FILING DATE: 2000-03-18 NUMBER OF SEQ ID NOS: 92
                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 419
TYPE: PRT
ORGANISM: Drosophila melanogaster
   183
                                                                        131
                                                                                                            153
                                    213 IIQVTSFLFYLLPMTVISVLYYLMALRV 240
                                                                                                                                                71
                                                                                                                                                             93 LLGMPLEVYEMWRNYPFLEGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAK 152
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                                                                                                                                                                                                                 GPPRDPLAIVIPUTVVYSLIFITGVVGNISTCIVIKKNRSMHTATNYYLFSLAISDFLLL 70
--QLSTFIFFLAPMSIILVLYLLIGVHL 208
                                                                      | ||:||: :|| ::: ::| : ||: || || || ::: : ::| AMSKLSRAIRIIVLVWIMAIVTAIPQAAQFGIE-HY------SGVEQCGIVRVIVKHSF 182
                                                                                                        LQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPGSATCTVIKPMWIYNF 212
                                                                                                                                            85;
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                                                                                                                                                                                                                                                                                                              33.1%; Score 418; DB 10; 40.9%; Pred. No. 1e-32;
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CURRENT APPLICATION NUMBER: US/09/911,005
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 60/220,042
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 222
TYPE: PRT
                                                                                                                                                                                                                                                                                    APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 80090, 52874,52880,63497, ANI
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
FILE REFERENCE: 38155-20044,00
CURRENT APPLICATION NUMBER: US/10/080,960
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,040
PRIOR APPLICATION NUMBER: US 60/242,038
PRIOR APPLICATION NUMBER: US 60/242,038
PRIOR APPLICATION NUMBER: US 60/242,038
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                                                                                                            SEQ ID NO 25
LENGTH: 259
                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/241,992
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/242,637
PRIOR FILING DATE: 2000-10-23
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity
Matches 67; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Millennium Pharmaceuticals, APPLICANT: Glucksmann, Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Glucksmann, maria Alexandra TITLE OF INVENTION: 65494, A NOVEL HUMAN G-PROTEIN-COUPLED TITLE OF INVENTION: RECEPTOR FAMILY MEMBER AND USES THEREC FILE REFERENCE: 10448-076001
OTHER INFORMATION: Consensus amino acid sequence 10-080-960-25
                                        TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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64;
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OF HUMAN PROTEINS AND USES THEREOF
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CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 60/246,768
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR FILING DATE: 2000-11-18
PRIOR FILING DATE: 2000-11-15
PRIOR FILING DATE: 2000-11-15
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Best Local Similarity
Matches 67; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Leiby, Kevin R.
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: 1625204900
FILE REFERENCE: 38155204900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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175
                                   224 LPMTVISVLY
                                                                       116 LLLSLPPLLFSWVKTVEEGNGTLNVNVTVCLIDFPEESTASVSTWLRSYVL-LSTLVGFL 174
                                                                                                       172 VLFSLPNTSIHGIKFHYFPNGSLVPGSATCTVIKP------MWIYNFIIQVTSFLFYL 223
                                                                                                                                                                     113 PVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTR-RRALRILGIVWGFS 171
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LPLLVILVCY 184
                                                                                                                                                                                                                           GNLLVILVILRTKKLRTPTNIFILNLAVADLLFLLTLPPWALYYLVGGSEDWP-----FG 55
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35.3%;
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Pred. No. 4.7e-18;
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Pred. No. 4.7e-18;
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CURRENT APPLICATION NUMBER: US/10/077,698
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 09/261,599
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-07-761
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: 09/223,538
PRIOR APPLICATION NUMBER: 09/223,538
PRIOR APPLICATION NUMBER: 09/223,538
PRIOR APPLICATION NUMBER: 09/223,538
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 259
LENGTH: 259
TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 259
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10077698 Publication No. US20030008350A1 GENERAL INFORMATION:
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APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 38650, 28472, 5495,
TITLE OF INVENTION: 14354 METHODS AND
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 14273 Receptor, A No. US20030008350Alel G-Protein Coupled Receptor FILE REFERENCE: 5800-4B, 035800/177086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/246,772
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR FILING DATE: 2000-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 381552004900
CURRENT APPLICATION NUMBER: US/10/012,140
CURRENT FILING DATE: 2001-11-08
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ORGANISM: Unknown
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US-09-796-338A-23
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 259
TYPE: PRT
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Patent No. US20020061522A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: MILLENTION: 52881, 2398, 45449, 50289, AND
TITLE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
FILE REFERENCE: 10448-020001
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                  172 VLFSLPNTSIHGIKFHYFPNGSLVPGSATCTVIKP-----MWIYNFIIQVTSFLFYL 223
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                                                                                                                                                          56 SALCKLYTALDVVNMYASILLLTAISIDRYLAIVHPLRYRRRRTSPRRAKVVILLVMVLA 115
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LPLLVILVCY
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Transmembrane Segment Rhodopsin
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35.3%;
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Pred. No. 4.7e-1
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US-09-823-114-20; Sequence 20, Application US/09823114

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
248
                                                                                                               170
                                                                                                                                                       137
                                   227 TVISVLYYLMALRV 240
                                                                           196
                                                                                                                                                                                     110 LFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWG 169
                                                                                                                                                                                                                                                 79 IVCVVGLEGNELVMYVIVRYTKMKTATNIYIENLALADALATST-LPEQSVNYLMGTWP- 136
                                                                                                                                                                                                                                                                                                           30
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                       8 SWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHF--------FLPVSVVYV 50
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FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
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MEDIUM TYPE: Floppy disk
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LIITVCYGLMILRL 261
                                                                       LSSAIGLPVMFMATTKYR
                                                                                                           FSVLFSLPNTSIHGIKFHYFPNGSLVPGSATCTVI--KPMWIYNFIIQVTSFLF-YLLPM 226
                                                                                                                                                 -FGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDFRTPRNAKIINVCNWI 195
                                                                                                                                                                                                                                                                                                       SWV-----NLSHLDGNLSDPCGPNRTNLGGRDSLCPPTGSPSMITAITIMALYS 78
                                                                                                                                                                                                                                                                                                                                                                                   72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: group(9, 12, 33, 40, 48)
OTHER INFORMATION: /note= "extracellular Asn residues
that are consensus sites for N-linked glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20526.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/823,114
FILING DATE: 29-Mar-2001
CLASSIFICATION: CURknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 3e-19; Mismatches
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                                                                       QGSIDCTLTFSHPTWYWENLVKICVFIFAFIMPV 247
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US-09-761-962-26
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APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: Identification and Characterization of Multiple Splice
TITLE OF INVENTION: Variants of Mu-
TITLE OF INVENTION: opioid Receptor (MOR-1) Gene
FILE REFERENCE: 830002-2000.1
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Memorial Sloan-Rettering Cancer Center
TITLE OF INVENTION: Identification and Characterization
TITLE OF INVENTION: Variants of Mu-
TITLE OF INVENTION: opioid Receptor (MOR-1) Gene
FILE REFERENCE: 830002-2000.1
                                                                                                                                                                                                                                                            SEQ ID NO 26
LENGTH: 391
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                                                                                                                        Best Local Similarity Matches 70; Conserv
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                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/761,962
CURRENT FILLING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/743,872
PRIOR FILING DATE: 2001-03-13
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SOFTWARE: PatentIn versi
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CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/743,872
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TYPE: PRT
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77 TNYYLFSLAVSDLLVLLLGMPLE-VYEMWRNYPFLFGPVGCYFKTALFETVCFASILSIT 135
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                                       CGPNRTGLGGSHSLCPQTGSPSMVTAITIMALYSIVCVVGLFGNFLVMYVIVRYTKMKTA 102
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Pred. No. 3.9e-17;
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Pred. No. 3.9e-17;
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
LENGTH: 392
Type: nom
                                                                                                                                                                                                                  Sequence 2, Application US/09214904 Patent No. US20010047519A1 GENERAL INFORMATION:
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APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: Identification and Characterization
TITLE OF INVENTION: Variants of Mu-
TITLE OF INVENTION: opioid Receptor (MOR-1) Gene
FILE REFERENCE: 830002-2000.1
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CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/743,872
PRIOR FILING DATE: 2001-03-13
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atent No. US20020077285A1
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                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/214,904
                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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APPLICATION DATA:
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Pred. No. 3.9e-17;
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; ORGANISM: Mus musculus US-09-761-962-29
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US-09-761-962-29
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APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: Identification and Characterization
TITLE OF INVENTION: Variants of Mu-
TITLE OF INVENTION: Opioid Receptor (MOR-1) Gene
FILE REFERENCE: 830002-2000.1
CURRENT APPLICATION NUMBER: US/99/761,962
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/743,872 PRIOR FILING DATE: 2001-03-13
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LENGTH: 398 amino acids
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                                                                                                                                 TNIYIFNLALADALATST-LPFQSVNYLMGTWP--FGNILCKIVISIDYYNMFTSIFTLC 159
                                                                                                                                                                                                       CGPNRTGLGGSHSLCPQTGSPSMVTAITIMALYSIVCVVGLFGNFLVMYVIVRYTKMKTA 102
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Pred. No. 4e-17;
""smatches 84;
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В

212 QGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITVCYGLMILRL 259

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-645-83
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US-09-966-871-83
Query Match
Best Local Similarity
Matches 70; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 83, Application US/10039645 Patent No. US20020147170A1
                                                                                                                                                                                                                                           APPLICANT: Ropin, Alan S.
APPLICANT: Beinborn, Martin
TITLE OF INVENTION: Constitutively Active, Hypersensitive,
TITLE OF INVENTION: and No. US20020147170Alfunctional Receptors as No. US20020147170
FILE REFERENCE: 00398/510002
CURRENT APPLICATION NUMBER: US/10/039,645
CURRENT FILING DATE: 2001-10-25
CURRENT FILING DATE: 2001-10-25
CURRENT FILING DATE: 2001-10-25
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PRIOR FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kopin, Alan S.
TITLE OF INVENTION: Assays for Identifying Receptors Having
TITLE OF INVENTION: Alterations in Signaling
FILE REFERENCE: 00398/512002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
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QGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITVCYGLMILRL 259
                                                                                                                                      TNIYIFNLALADALATST-LPEQSVNYLMGTWP--FGNILCKIVISIDYYNMFTSIFTLC 159
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                                 PGSATCTVI - - KPMWIYNFIIQVTSFLF - YLLPMTVISVLYYLMALRV 240
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Search completed: January 17, 2003, 05:09:27 Job time: 67 secs

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Run
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Compugen Ltd.
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BI224313	вJ499680	AK020259	BE266564	AK005368	вв656301	BI872266	BE746231	BB642318	BH160272	AZ548467	AZ551618	BE654347	CNS04SGJ	BF446062	BI600170	BI873140	BB642387	в1753905	BG714306	BM546496	AK004891	BC018330	BI463235	BM808823	BM808829	BI757121	BM925480	CNS020N1	CNSOSORV	BF323227	BM543497	BF603623	CNS01xJ2	CNS04GXP	AU244285	AU244292	CNS036WH	в0721315
BI224313 602940621	0896)259	5564	5368	5301	2266	5231	2318)272	3467	1618	1347	5164	5062)170	3140	2387	3905	1306	5496	1891	3330	3235	3823	3829 A	7121 6	5480 A	19494	300	3227 m	3497 A	3623 2	1767 T)230 T	285 AU	44292 AU	30570 T	721315 AC

ALIGNMENTS

TITLE JOURNAL COMMENT ACCESSION VERSION KEYWORDS SOURCE ORGANISM FEATURES REFERENCE DEFINITION Locus AUTHORS source sequence. BM737726 BM737726.1 Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 16 row: A column: 04
High quality sequence stop: 540. Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 540)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Unpublished (2002) Contact: Kim YS BM737726 K-EST0000769 S1SNU5 Homo 21C Frontier Korean EST Project 2001 GI:19059055 540 bp mRNA linear EST 01-MAR-2002 sapiens cDNA clone S1SNU5-16-A04 5', mRNA

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RESULT 2
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               DEFINITION
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            Pan
                                       AG046172
      troglodytes
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/db_xref="taxon:9606"
/clone="S1SNU5-16-A04"
/clone_lib="S1SNU5"
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/cell_line="SNU-5"
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/tissue_type="Ascites"
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99.8%;
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         clone:
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Pred. No. 1.7e-110;
   670 bp DNA
ne: PTB-025E24.R,
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      survey
                              GSS 02-NOV-2001
      sequence
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                                                                                                                                                                                                            CAACACCAGCATCCATGGCATCAAGTTCCACTACTTCCCCAATGGGTCCCTGGTCCCAGG
                                                                                                                                                                                                                                                                                                                                                CCTGGAGGTCTATGAGATGTGGCGCAACTACCCTTTCTTGTTCGGGCCCGTGGGCTGCTA
                                                                  CAACACCAGCATCCATGGCATCAAGTTCCACTACTTCCCCAATGGGTCCTTGGTCCCAGG
                                                                                                                                                         GCGCCGGCCCTCAGGATCCTCGGCATCGTCTGGGGCTTCTCCCGTGCTCTTCTCCCTGCC
                                                                                                                                       GCGCCGGGCCCTCAGGATCCTCGGCATCGTCTGGGGGCTTCTCCGTGCTCTTCTCCCTGCC
                                                                                                                                                                                                                                                                               CTTCAAGACGGCCCTCTTTGAGACCGTGTGCTTCGCCTCCATCCTCAGCATCACCACCGT
                                                                                                                                                                                                                                                                                                 CTTCAAGACGGCCCTCTTTGAGACCGTGTGCTTCGCCTCCATCGTCAGCATCACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                    CAACTACTACCTCTTCAGCAGGGCGGTCTCTGACCTCCTGGTACTGCTCCTTGGAATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone tracking errors.
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Totoki,Y., Watanabe,H. and Sakaki,Y
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAC end sequences of Library
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AG046172.1
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R.Site 1
R.Site 2
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/clone_lib="PTB Chimpanzee Male
157 c 213 g 138 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Pan troglodytes"
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98.6%;
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Pred. No. 2.1e-101;
0; Mismatches 7;
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                                                   AAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGGACCTCGGCGCAGCCAC 120
                                  AAATACCTGAACAACACAGATGACTACCTAGCTTTGCTCTGCGGGCCTCGTCGCAGCCAC
                                                                                                     ATGGAAAAACATGAGAATGTTTCCTGGATGTACCAACAGGAACTGAAAGATCCTTTCAAG 168
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BE751626
BE751626.1 GI:10165618
EST.
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Flate: 44 row: O column: 6
Seq primer: ATTTAGGTGCACGTATAG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
Single pass sequencing. Bases cal
v0.980904.e. Vector identified by
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cow.
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                             adrenal, and endometrium."
165 c 134 g 156 t
                                                                                                                                                                                                                                                                                   /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sa Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal and endometrium."
                                                                                                                                                                                                                                                                                                                                                    /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="MARC 2BOV"
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1 ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG

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REFERENCE
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 481;
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (1999)
                                                                                                                                                                                                                                                                                         High quality sequence start: 11
High quality sequence stop: 602.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               Plate: LLAM9573 row: p column: High quality sequence start: 11
                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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BE871983
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                                                                                      186
 Conservative
                                                                                                    /Clone="IMAGE:3852151"
/clone_lib="NIH_MGC_65"
/clone_lib="NIH_MGC_65"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sali; Cloned unidirectionally. Primer: Oligo d
Average insert size 1.8 kb. Library constructed by Li
Technologies. "
                                                                                    Technologies. "
252 c 228
                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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                43.2%;
85.4%;
Score 315; DB Pred. No. 1.1e 0; Mismatches
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTCCTGGTGTGCCTGGTGATCCTGCAGCACCAGGCTATGAAGACGCCCACCAA-TACTA 380
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                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                               Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., K., M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sa,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H. Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya, Muramatsu,M. and Hayashizaki,Y.
  Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibatta,Y., Hayatsu,N,
,M., Konno,H., Okazaki,Y., Muramat:
                                                                                                                                                                                                                                                      Unpublished (2001)
On Nov 30, 2000 this sequence version replaced gi:11483994
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 624)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara,
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BB587450
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BB587450
BB587450.2 GI:16449720
                                                                                                        Fax: 81-45-503-9216
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RIKEN full-length enriched, adult female vagina
cDNA clone 9930001G13 5', mRNA sequence.
Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,. Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                   RIKEN Genomic
                          Shibata, K.,
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1 ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG 60 ATGGGAAAACTTGAAAATGCTTCCTGGATCCAC-------GATTCTCTCATG 150

Mismatches

16;

Gaps

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151 AAGTACTTGAACAGCACAGAGGAGTACTTGGCCTACCCTGTGTGGACCCAAGCGCAGTGA

210

AAACACCTGAACAGCACCGAGGAGTATCTGGCCT-TCCTCTGCGGACCTCGGCGCAGCCA 119

CCTATCCCTTCCAGTGTCTGTGGTCTATGCGCTGATCTTCGTGGTGGGGGGTGATAGGCAA CTTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGTCATTGGCAA 179 Best Loc Matches

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al Similarity 373; Conser

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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Hayashizaki,Y.
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Y. and Hayashizaki,Y.
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/dev_stage="adult"
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/db_xref="taxon:10090"
/clone="9930001G13"
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Bos taurus
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Tel: 40
Fax: 40
                                                                                                                                                                                                                                                                                                                                                             Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G. Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
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203132 MARC 2BOV Bos taurus
BE751310
BE751310.1 GI:10165239
EST.
                                                                                                                                                                                                                                and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov
Single pass sequencing. Bases cal
v0.980904.e. Vector identified by
and _minmatch 12 options.
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402 762 4390
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Library made from pooled tissue from testis,
semitendonosus muscle, longissimus muscle, p
                                                                                             /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
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                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 993) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
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/note="Vector: pCMV-SPORT6 (Life Technologies); Si NotI; Site_2: SalI; cDNA made by Oligo dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and
                                                                      /tissue_type="sympathetic
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6194542"
                                                                                                                         /sex="male"
                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                              /clone_lib="Lupski_sympathetic_trunk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:21860212
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                                                 Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetier,F., Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                          GSS; genome survey sequence
Tetraodon nigroviridis.
Tetraodon nigroviridis
                                  Tetraodon nigroviridis
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Tetraodontiformes;
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  of library G from Tetra
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1 26 c 308 g 198 t 1 others
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                       AU244292
AU244292 Medaka eye cDNA library (SNKO1) Oryzias latipes cDNA clone NGY47.02e similar to pir|T15816|hypothetical protein C48C5.1 - Caenorhabditis elegans, mRNA sequence.
AU244292
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This sequence is a single read and was generated scale clone-end sequencing project of the Tetraod genome. For more information, please take a look http://www.genoscope.cns.fr/Tetraodon.
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Direct Submission
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/db_xref="taxon:99883"
/clone="216F22"
/clone_lib="G"
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177 c 327 g 132 t 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Biological Sciences Graduate School of Science, Nagoya University Furo-cho, Chikusa-ku, Nagoya 464-8602, Japan Tel: 81-52-789-2973
Fax: 81-52-789-2974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sanaka,E., Hori,H., Naruse,K., Mitani,H. and Tanaka,M. Medaka EST analysis Unpublished (2001)
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clone was isolated from Medaka
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Oryzias latipes"
/strain="wild type"
/db_xref="taxon:8090"
/clone="NGY47.02e"
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/tissue_type="eye"
/dev_stage="adult"
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clc 109K06 of library G from Tetraodon nigroviridis, genomic survey sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos:
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos:
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neotele:
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: sanaka@bio.nagoya-u.ac.jp
This clone was isolated from Medaka
Location/Qualifiers
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Contact: Emi Sanaka
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Sanaka, E., Hori, H., Naruse, K., Mitani, H. and Tanaka, M.
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/strain="wild type"
/db_xref="taxon:8090"
/clone="NGY47.01f"
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/tissue_type="eye"
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GGCCCTCAGGATCCTCGGCATCGTCTGGGGGCTTCTCCGTGCTCTTCTCCCTGCCCAACAC
                                                                                                         GGAGCGCTACGTGGCCATCCTACACCCGTTCCGCGCCAAACTGCAGAGCACCCGGCGCCG
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at
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http://www.genoscope.cns.fr/Tetraodon
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fizameau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A.
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GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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Roest-Crollius,H., Jaillon,O., Dasi
Bernot,A., Fizames,C., Wincker,P.,
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/clone_lib="G"
/note="Genoscope sequence
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ACKTCTCCTGTAAGATCTACAACTTCCTGTTCGAG-GCGTGCAGTACGCCACCATTGTGA
                                                                                                                      TTGGAATGCCCCTGGAGGTCTA---TGAGATGTGGCGCAACTACCCTTTCTTGTTCGGGC
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Tetraodon nigroviridis
Tetraodon nigroviridis
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Direct Submission
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1 (bases 1 to 817)

Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,

Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F.,
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/note="Genoscope sequence ID : COAG202CC12SP1-end PUC-Ori"
237 c 258 g 159 t 5 others
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/db_xref="taxon:99883"
/clone="202F23"
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Pred. No. 2.5e-14;
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                    CCTGGTGATTCTGCAGCACCAGGCTATGAAGACGCCCACCAACTACTACCTCTTCAGCCT
                                                      CGTCACAGCCACCTGCGTGGCGCTCTTCGTGGTGGGCATCGCGGGCAACCTGCTCACCAT 126
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BF603623.1 GI:11701421
EST.
Cow.
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence evaluation of four pooled-tissue normalized bovine libraries and construction of a gene index for cattle
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269181 MARC 3BOV Bos taurus
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
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primer: ATTTAGGTGACACTATAG.
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                                                                                                                            Conservative
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                                                                                                                                                                                                             /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: Sall;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
                                                                                                                                                                                                                                                                                                                                           /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
                                                                                                                                                                                                                                                                                                        /tissue_type="pooled"
/lab_host="DH10B"
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Ruminantia; Pecora;
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                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12719 row: e column: 24
High quality sequence stop: 635...
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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1 (bases 1 to 1027)
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    153
                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5726591"
/clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
                 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: ECORV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012.
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Query Match
Best Local Similarity

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BF323227
BF323227.1
EST.
house mouse.
MGI:1455149
Seq primer:
                                                               (CGAP/BTGAP), Tumor Gene Index (1998)
Other_ESTS: maa38a07.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                            Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; la Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; la 448)

1 (bases 1 to 448)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
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448 bp mrNA linear EST 21-NOV-2000 maa38a07.yl NCI_CGAP_Brn63 Mus musculus cDNA clone IMAGE:3813037 5' similar to SW:NTR2_RAT Q63384 NEUROTENSIN RECEPTOR TYPE 2 ;, mRNA
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1:
Site_2: Sall; Cloned unidirectionally. Primer: Ol
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·		Sequence 9, Appli Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 628, App Sequence 627, Appli Sequence 7, Appli Sequence 9, Appli Sequence 18, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 16, Appli Sequence 17, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 17, Appli Sequence 18, Appli Sequence 17, Appli Sequence 18, Appli Sequence 17, Appli Sequence 18, Appli Sequence 17, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli

; ORGANISM: Drosophila melanogaster; FEATURE: FAME/KEY: CDS; LOCATION: (1)..(1257)
US-09-804-551B-25 밁 δõ DЬ οy 밁 Ş DЬ Matches 241; Query Match Best Local Similarity 234 300 174 240 114 180 120 54 CATAAGTACCTGCATTGTGATTAAGAAGAACCGTTCAATGCACACGGCCACGAATTACTA CTTCTTCCTCCCCGTGTCTGTGGGTGTATGTGCCAATTTTTTGTGGTGGGGGGTCATTGGCAA 179 GTCCTACATCTGGTCCAAGTACCCGTACGTGTTTGGGGGAGTACATCTGCATCGGACGTGG CTATGAGATGTGGCGCAACTACCCTTTCTTGTTCGGGCCCGTGGGCTGCTACTTCAAGAC CCTCTTTTCGCTGGCATCTCGGATTTCCTGCTCCTGTTGTCGGGCGTTCCGCAGGAGGT CCTCTTCAGCCTGGCGTCTCTGACCTCCTGGTCCTGCTCCTTGGAATGCCCCTGGAGGT CATCGTGATACCCGTAACGGTGGTCTACTCCCTCATTTTCATAACCGGTGTAGTGGGCAA Conservative 16.48; Score 119.8; DB 10; Pred. No. 1.9e-21; 0; Mismatches 202; Indels Length 1258; 0; Gaps 113 293 233 299 173

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 325
SOFTWARE: PatentIn version 3.0
SEQ ID NO 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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APPLICANT: Augustus, Meena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 296, Application US/09967768A Patent No. US20020150877A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signaturitle OF INVENTION: Sets
FILE REFERENCE: 689290-72
CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT FILING DATE: 2001-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US/60/236,034
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,111
PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/967,768A CURRENT FILING DATE: 2001-09-28 PRIOR APPLICATION NUMBER: US/60/236,109 PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1427
                                                                                                                                                        490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                 GGGGCTTCTCCGTGCTCTTCTCCCTGCCCAACACCAGCATCCATGGCATCA
                                                                          CTCTGCGCGCGGCGACCTACCGGCGGGCCCAGCGTGGCCAAGCTCATCAACCTGGGCGTGT
                                                                                                                                                                                    TCGCCTCCATCCTCAGCATCACCGTCAGCGTGGAGCGCTACGTGGCCATCCTACACC 442
                                                                                                                                                                                                                                                                                                                                                                                                     TGCAGCAGCAGGCTATGAAGACGCCCACCACTACTACCTCTTCAGCCTGGCGGTCTCTG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTATGTGCCAATTTTTGTGGTGGGGGTCATTGGCAATGTCCTGGTGTGCTGCTGGTGATTC 202
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                                                                                                             CGTTCCGCGCCAAACTGCAGAGCACCCGGCCCCGGCCCTCAGGATCCTCGGCATCGTCT 502
                                                                                                                                                  TCACCAGCGTCTTCTGTCTCACCGTGCTCAGCGTGGACCGCTACGTGGCCGTGGTGCACC
                                                                                                                                                                                                                             C----CTTCGGCTCCGTGCTGTGCCGCGCGGTGCTCAGCGTCGACGGCCTCAACATGT
                                                                                                                                                                                                                                                              CTTTCTTGTTCGGGCCCGTGGGCTGCTACTTCAAGACGGCCCTCTTTGAGACCGTGTGCT
                                                                                                                                                                                                                                                                                                     ACGAGCTCTTCATGCTGAGCGTGCCCTTCGTGGCCCTCGTCGGCCCCCTGCGCCACTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATTCGCATCATCGTCCTGGTTTGGATTATGGCCATAGTTACGGCCATTCCGCAGGCTGC 473
                                                                                                                                                                                                                                                                                                                                          ACCTCCTGGTCCTGCTCCTTGGAATGCCCCTGGAGGTCTATGAGATGTGGCGCAACTACC 322
                                                                                                                                                                                                                                                                                                                                                                                TTCGCTACGCCAAGATGAAGACGGCTACCAACATCTACCTGCTCAACCTGGCCGTAGCCG
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Pred. No. 1.4e-14;
0; Mismatches 185; Indels
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APPLICANT: XU, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Filing, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSTS OF OVARIAN C?
FILE REFERENCE: 210121.484C5
CÜRRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
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                                                                                                                                                                                                                       Sequence 208, Application US/09825294 Patent No. US20020004491A1
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LENGTH: 1362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 210121.484C6
CURRENT APPLICATION NUMBER: US/09/970,966
CURRENT FILING DATE: 2001-10-02
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SOFTWARE: FastSEQ for Windows Version
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                          497
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Molesh, David,
Fling, Steven
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P.
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OVARIAN CANCER

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APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 TGGGGGTCATTGGCAATGTCCTGGTGTGCCTGGTGATTCTGCAGCACCAGGCTATGAAGA 223
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                            AGAGCACCCGGGCCCGGGCCTCAGGATCCTCGGCATCGTCTGGGGCTTCTCCGTGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCCCACCAACTACCTCTTCAGCCTGGCGGTCTCTGACCTCCTGGTCCTGCTTC 283
                                                                                                                                                                      TCACCACCGTCAGCGTGGAGCGCTACGTGGCCATCCTACACCCGTTCCGCGCCAAACTGC
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                                                                                                                               TGCTGACACTCAGCTTTGAGCGCTACATCGCCATCTGTCACCCCTTCAGGTACAAGGCTG
                                                                                                                                                                                                                                                                  TGTCCTGCAAGCTGCACACTTTCCTCTTCGAGGCCTGCAGCTACGCTACGCTGCACG
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TGTCGGGACCTTGCCAGGTGAAAGCTGCTGATTTGGCTTCGTCTGGGTCACCTCCGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGAGGTGACAGACCACATGGTGAGTTTGGCTTGCTCGGACATCTTGGTGTTCCTCATCG
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496
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: LOCATION: (135)...(1454)
: NAME/KEY: misc_feature
: LOCATION: (1)...(1647)
: OTHER INFORMATION: n = A,T,C
US-09-829-631A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-829-631A-12
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/829,631A CURRENT FILING DATE: 2001-04-10 PRIOR APPLICATION NUMBER: US 08/428,242 PRIOR FILING DATE: 1995-09-18 NUMBER OF SEO ID NOS: 13 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO
LENGTH:
                               Query Match
Best Local Similarity
Matches 200; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09829631A
Patent No. US/0020091235A1
EENERAL INFORMATION:
APPLICANT: Sibley, David R.
APPLICANT: Monsma, Frederick J.
APPLICANT: Hamblin, Mark
TITLE OF INVENTION: The ST-B17 Serotonin Receptor
FILE REFERENCE: NIH047.1CPLC1
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Best Local S
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SEQ ID NO 208
LENGTH: 1362
                                                                                                                                                                                                 NAME/KEY: CDS
                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                         TYPE: DNA
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158 TTGTGGTGGGGGTCATTGGCAATGTCCTGGTGTGCCTGGTGATTCTGCAGCACCAGGCTA 217
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                                     Conservative
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                                 Score 85.6; DB 10;
Pred. No. 1.1e-12;
0; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 89.4; DB 10; Pred. No. 1.1e-13;
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                                                                   Length 1647;
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                                                                 US-09-917-800A-1620
                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1620
LENGTH: 2108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1620, Application US/09917800A Patent No. US20020119462A1
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/917,80 CURRENT FILING DATE: 2001-07-31 PRIOR APPLICATION NUMBER: US 60/222,040 PRIOR FILING DATE: 2000-07-31 PRIOR APPLICATION NUMBER: US 60/222,880 PRIOR APPLICATION NUMBER: US 60/222,880 PRIOR FILING DATE: 2000-11-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mendrick, Donna APPLICANT: Porter, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/290,029 PRIOR FILING DATE: 2001-05-11
                                                                                                                           ORGANISM: Rattus norvegicus
                                                                                                                                                    TYPE: DNA
                                                                                     OTHER INFORMATION:
                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478
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                                                                                                                                                                                                                                                                                                                                          OR APPLICATION NUMBER: US 60/290,645
OR FILING DATE: 2001-05-15
OR APPLICATION NUMBER: US 60/292,336
OR FILING DATE: 2001-05-22
OR APPLICATION NUMBER: US 60/295,798
OR FILING DATE: 2001-06-06
OR APPLICATION NUMBER: US 60/297,457
OR FILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/298,884 FILING DATE: 2001-06-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnson, Kory
Castle, Arthur
Elashoff, Michael
                                                                                     Genbank Accession No.
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11.3%;
47.5%;
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Score 82.6; DB 10; Pred. No. 7e-12;
                                                                                   US20020119462A1 NM_016991
                    Length 2108;
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Matches

278;

149

246

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; LOCATION: (1)..(1341); OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein US-10-077-870-1
                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 3.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10077870 Publication No. US20030003470A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/077,870 CURRENT FILING DATE: 2002-05-21 PRIOR APPLICATION NUMBER: FI 20010323 PRIOR FILING DATE: 2001-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a
FILE REFERENCE: 0933-0183P
                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 10
  170 TCATTGGCAATGTCCTGGTGTGCCTGGTGAATTCTGCAGCACCAGGCTATGAAGACGCCCA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                546 TGGCATCAAGTTCCACTACTTCCCCAATGGGTCCCTGGTCCCAGGTTCGGCCACCTGTAC
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                                                                        Conservative
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                                                                                         Score 82; DB 9;
Pred. No. 8.5e-1;
                                                                   Mismatches
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                                                                                                           Length 1344
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                                                                                                                                                                ; LUCATION: (1)..(1341)
; OTHER INFORMATION: Coding sequence for variant;
; OTHER INFORMATION: alpha-2B-adrenoceptor proteius-09-825-923-1
    DЬ
                                         QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-09-825-923-1
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                                                                                       Matches 206;
                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09825923 Patent No. US20010016338A1
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: Drotein, and uses thereof
TILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION UMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                        170 TCATTGGCAATGTCCTGGTGTGCCCTGGTGAATTCTGCAGCACCAGGCTATGAAGACGCCCA 229
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CGCCCCTCATCTACAAGGGCGACCAGGGCCCCCA 470
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Karvonen, Matti
Koulu, Markku
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Nyyss″nen, Kristiina
Salonen, Riitta
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Scheinin, Mika
Salonen, Jukka T
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                                                                                     Conservative
                                                                                                       11.2%;
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                                                                                                       Score 82; DB 10;
Pred. No. 8.5e-12;
                                                                                   Mismatches
                                                                                                                                                                                          protein
                                                                                                                          Length 1344;
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US-10-077-870-1

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Query Match
Best Local Similarity

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TYPE: DNA ORGANISM: Homo NAME/KEY: CDS FEATURE:

LENGTH: 1344

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Sequence 3, Application US/10077870

Publication No. US2003003470A1

GENERAL INFORMATION:

APPLICANT: Salonen, Jukka T

FILE REFERENCE: 0933-01839

CURRENT APPLICATION NUMBER: US/10/077,870

CURRENT FILING DATE: 2002-05-21

PRIOR APPLICATION NUMBER: FI 20010323

PRIOR FILING DATE: 2001-02-20

NUMBER OF SEQ ID NOS: 10
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, NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein US-10-077-870-3
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US-10-077-870-3
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Best Local Similarity
Matches 206; Conserv
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TYPE: DNA
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                   TCAGCGTGGAGCGCTACGTGGCCATCCTACACCCGTTCCGCGCCAAACTGCAGAGCACCC
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TCAGCCTGGACCGCTACTGGGCCGTGAGCCGCGCGCTGGAGTACAACTCCAAGCGCACCC
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0; Mismatches
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8.6e-12;
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US-09-825-923-3
; Sequence 3, Application US/09825923
; Patent No. US20010016338A1
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LENGTH: 1353
TYPE: DNA
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Best Local Similarity
Matches 206; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding se
OTHER INFORMATION: protein
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APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: A protein, and uses thereof
TILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
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                                    410 TCAGCGTGGAGCGCTACGTGGCCATCCTACACCCGTTCCGCGCCAAACTGCAGAGCACCC 469
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ACTTCAAGACGGCCCTCTTTGAGACCGTGTGCTTCGCCTCCATCCTCAGCCATCACCACCG 409
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Alhopuro, Pia
Karvonen, Matti
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Nyyss"nen, Kristiina
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Salonen, Jukka T
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                                                                                                                                                                                                                                                                                                                                                                      DB 10;
8.6e-12
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CURRENT FILING DATE:

2002-01-18

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US-10-052-589-1
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US-10-044-090-444
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        GENERAL INFORMATION:
APPLICANT: Perez, Dianne
APPLICANT: Zuscik, Michael
APPLICANT: Zuscik, Michael
TITLE OF INVENTION: Model systems for neurodegenerative and cardiovascular disorders
FILE REFERENCE: 26473/04200
FILE REFERENCE: 26473/04200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 444
LENGTH: 2487
TYPE: DNA
                                                                                             Sequence 1, Application US/10052589 Patent No. US20020133832A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES [
FILE REFERENCE: PA-0028 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 444, Application US/10044090 Patent No. US20020137081A1
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    CURRENT APPLICATION
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CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
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                                                                                                                                                                                                                                     CTGGGTGCTGTCGTTTGCCATCGGCCTGACTCCCA
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    NUMBER:
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US/10/052,589
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Pred. No. 6.2e-11;
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US-09-964-824A-249
; Sequence 249, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
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TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-73
CURRENT APPLICATION NUMBER: US/09/964,824A
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236,033
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR FILING DATE: 2000-09-28
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                                                                                                                                APPLICANT: Horrigan, Stephen
TITLE OF INVENTION: Cancer Gene Determination
TITLE OF INVENTION: Sets
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TYPE: DNA
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nes 275; Conserv
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Pred. No. 1.
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PRIOR PRIOR

APPLICATION NUMBER: US/60/236,028 FILING DATE: 2000-09-28

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; NAME/KEY: CDS
; LOCATION: (91)..(1176)
US-09-940-240-15
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Query Match
Best Local Similarity
                                                                                                                                                                     NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 15
LENGTH: 2050
                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/09940240 Patent No. US20020166133A1
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Best Local Similarity
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SOFTWARE: PatentIn version
SEQ ID NO 249
LENGTH: 2595
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                                                                                                                                                                                                                                                              FILE REFERENCE: MBIO98-008CPICNIM
CURRENT APPLICATION NUMBER: US/09/940,240
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09/248,239
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 09/023,664
PRIOR FILING DATE: 1008-02-08
                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NEOKINE PROTEIN AND TITLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1998-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Millennium Pharmaceuticals,
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 995, Application US/09954531 Patent No. US20020165180A1
               SOFTWARE: PatentIn version SEQ ID NO 995
                                                                  PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using TITLE OF INVENTION: Gene Sets FILE REFERENCE: 689290-77
                                             WILLOW FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
                                                                                                                                                                               PRIOR APPLICATION NUMBER: US/60/234,009 PRIOR FILING DATE: 2000-09-20
                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US/60/233,133 PRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/954,531
LENGTH: 2625
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1: sp_archea:*
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5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
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12: sp_virus:*
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Q9jibl rattus norv
Q9hb89 homo sapien
Q9jibl rattus norv
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                 Q9vfn4 drosophila
Q9vfw6 drosophila
Q9vfw5 drosophila
Q9vfw5 drosophila
Q18701 caenorhabdi
017239 caenorhabdi
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Q96am5 homo
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9 caenorhabdi
12 sphoeroides
13 sphoeroides
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ALIGNMENTS

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RESULT 1

O9GZQ4

ID

O9GZQ4: O9NRA6;

AC

O9GZQ4: O9NRA6;

DT

O1-MAR-2001 (TrEMBLrel. 16, Created)
DT

O1-MAR-2001 (TrEMBLrel. 21, Last sequence update)
DT

O1-MAR-2001 (TrEMBLrel. 21, Last sequence update)
DT

O1-JUN-2002 (TREMBLrel. 21, Last annotation update)
DT

O1-MAR-2001 (TREMBLrel. 21, Last annotation update)
DT

Neuromedin U receptor TGR-1.

OS

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho

NCBI_TaxID-9606;
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R1

SEQUENCE FROM N. A.

RX

MEDLINE-20490668; PubMed-10899166;
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RA

MEDLINE-20490668; PubMed-10899166;
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MEDLINE-20490668; PubMed-10899166;
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MEDLINE-20490668; PubMed-10899166;
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MEDLINE-20490668; PubMed-10899166;
RA

RA

MEDLINE-20490668; PubMed-10899166;
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Shan L., Qiao X., Crona J.H., Behan J., Wang S., Laz T., Bayne M., Gustafson E.L., Monsma F.J. Jr., Hedrick J.A.;
"Identification of a Novel Neuromedin U Receptor Subtype Expressed the Central Nervous System.";
J. Biol. Chem. 275:39482-39486(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raddatz R., Wilson A.E., Artymyshyn R., Bonini J.A., Borowsky B., Boteju L.W., Zhou S., Kouranova E.V., Nagorny R., Guevarra M.S., Boai M., Lerman G.S., Vaysse P.J., Branchek T.A., Gerald C., Forra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification and Characterization of Two Neuromedin
                                                                                                      EMBL/GenBank/DDBJ databases
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Best Local S
Matches 239
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Q96AM5;
Q96AM5;
O1-DEC-2001 (TrEMBLrel. 19
O1-DEC-2001 (TrEMBLrel. 19
O1-JUN-2002 (TrEMBLrel. 21
Neuromedin U receptor 2.
                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; E
Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ
EMBL; BC015938; AAH16938.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
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Pfam; pF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRHODOPSN.

PRINTS; PR01565; NEUROMEDINUR.

PRINTS; PR01567; NEUROMEDNUR.

PRINTS; PR01570; NEPFERCEPTOR.

PRINTS; PR01570; NEPFERCEPTOR.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Howard A.D., Wang R., Pong S.-S., Mellin T.N., Strack A., Guan X.-M., Zeng Z., Williams D.L., Feighner S.D., Nunes C.N., Murphy B., Stair J.N., Yu H., Jiang Q., Clements M.K., Tan C.P., Mckee K.K., Hreniuk D.L., Mcdonald T.P., Lynch K.R., Evans J.F., Austin C.P., Caskey T., van der Ploeg L.H.T., Liu Q.; "Identification of receptors for neuromedin U and its role in feeding.";
                                                                  SEQUENCE FROM
                                                    TISSUE=COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF272363; AAG24794.1; -. EMBL; AF292402; AAG03064.1; -. EMBL; AF242874; AAF82755.1; -. EMBL; AB041228; BAB13721.1; -.
                                                                                           NCBI_TaxID=9606
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J. Biol. Chem. 275:29528-29532(2000).
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Shintani Y., Fukusumi S., Habata Y.,
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                                                                                                     Eutheria;
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Last annotation updat
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                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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SEQUENCE
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PRINTS; PR01570; NEUROMEDNUR.
PRINTS; PR01570; NEFFRECEPTOR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization of murine neuromedin Submitted (SEP-2001) to the EMBL/GenBan EMBL, AY057384; AR126695.1; -
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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SEQUENCE
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PRINTS; PR01567; NEUROMEDNUZR.
PRINTS; PR01570; NEFERECEBETOR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gustafson E.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuromedin U receptor type Mus musculus (Mouse).
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ALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS
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                                           LLVCLVIARHQTLKTPTNYYLFSLAVSDLLVLLLGMPLEVYELWHNYPFLFGPVGCYFKT
                                                                                                                                           MGKLENASWIH-----DSLMKYLNSTEEYLAYLCGPKRSDLSLPVSVVYALIFVVGVIGN
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81.7%;
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Last annotation update)
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1; Mismatches
                                                                                                                                                                                                                                                                     Pred. No. 4.5e-89;
                                                                                                                                                                                                                                                                                         Score 1039.5;
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                                                                                                                                                                                                                                                                                                                                            0BB540024566903D CRC64;
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Best Loc
Matches
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Pfam; PF00001; 7tm_1; 1.

PRINTS: PR00237; GPCRRHODOPSN.

PRINTS: PR01565; NEUROMEDINUR.

PRINTS: PR01567; NEUROMEDINUR.

PRINTS: PR01567; NEUROMEDINUR.

PRINTS: PR01570; NEFFRECEPTOR.

PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UN

PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
                            Q9JIB1
Q9JIB1;
Q1-OCT-2000
Q1-OCT-2000
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                        Receptor.
SEQUENCE
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01-MAR-2001 (TrEMBLrel. 16, Creat
01-MAR-2001 (TrEMBLrel. 16, Last
01-JUN-2002 (TrEMBLrel. 21, Last
G protein-coupled receptor TGR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                      Neuromedin U Receptor.";
J. Biol. Chem. 275:29528-29532(2000).
EMBL; AB041229; BAB13722.1; -.
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Hosoya M., Moriya T., Kawamata Y., Ol
Shintani Y., Fukusumi S., Habata Y.,
           Neuromedin
NMU2R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fujino M.;
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norvegicus (Rat)
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                   G
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                  O (TrEMBLrel. (TrEMBLrel. U receptor 2.
                                                 (TrEMBLrel.
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                             Last sequence update)
Last annotation updat
                                                 Created)
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Sciurognathi;
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Hinuma S.,
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thi; Muridae; Murinae; Rat
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Best Local
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                     Differentially System.";
J. Biol. Chem.
                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=20490668; PubMed=10899166;
MEDLINE=20490668; PubMed=10899166;
Raddatz R., Wilson A.E., Artymyshyn R., Bonini J.A
Boteju L.W., Zhou S., Kouranova E.V., Nagorny R.,
Boteju L.W., Zhou S., Vaysse P.J., Branchek T.A., (
                                                                                                                                                                                                                                                                                                                                                                                   O9HB89; O43664;
O1-MAR-2001 (TERMBLrel. 16, Created)
O1-MAR-2001 (TERMBLrel. 16, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Neuromedin U receptor 1 (Orphan G protein-coupled r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00237; GPCRHODOPSN.
PRINTS; PR01565; NEUROMEDINUR.
PRINTS; PR01567; NEUROMEDNU2R.
PRINTS; PR01570; NPFFRECEPTOR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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STRAIN-SPRAGUE-DAWLEY;

MEDLINE-20351041; PubMed-10894543;

Howard A.D., Wang R., Pong S.-S., Mellin T.N., Strack A., Guan X.

Zeng Z., Williams D.L., Feighner S.D., Nunes C.N., Murphy B.,

Stair J.N., Yu H., Jiang Q., Clements M.K., Tan C.P., Mckee K.K.,

Hreniuk D.L., Mcdonald T.P., Lynch K.R., Evans J.F., Austin C.P.,

Caskey T., van der Ploeg L.H.T., Liu Q.;

"Identification of receptors for neuromedin U and its role in
[2]
                                                                                                                                                                                                                                                                                                                                                                    NMUR1.
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Pfam; PF00001; 7tm_1; 1.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALFETVCEASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IHGIKFQHFPNGSSVPGSATCTVTKPMWVYNLIIQATSFLFYILPMTLISVLYYLMGLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALFETVCFASILSVTTVSVERYVAIVHPFRAKLESTRRRALRILSLVWSFSVVFSLPNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF242875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193;
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AF242875; AAF82756.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                     Expressed
                       275:32452-32459(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44722 MW;
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Rodentia;
                                                                                             Characterization
                                                                                                                                                                                                                                                                                                    Primates;
                                                                                                                                                                                                                                                                                                                       Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%;
                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                   Peripheral Tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1033.5;
Pred. No. 1.6e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                 Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01D3765B5D5355C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                     of Two Neuromedin
al Tissues and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426
                                                                                                                                                                                                                                                                                                                            Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNKNOWN_1.
                                                                                                                                                                                   Bonini J.A.,
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                                                                                                                                                                                                                                                                                                    Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                      , Guevarra M.
Gerald C., F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                           □
                                                                       Central Nervous
                                                                                             Receptors
                                                                                                                                        Forray
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                                                                                                                                        С.,
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RESULT 7
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Best Local
                                                                                                                                                                                                                                                                                          03/1B2;
01-OCT-2000 (TrEMBLrel. 1:
01-OCT-2000 (TrEMBLrel. 1:
01-JUN-2002 (TrEMBLrel. 2:
Nonromedin U receptor 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                               MEDLINE=20351041; PubMed=10894543;
Howard A.D., Wang R., Pong S.-S., Mellin T.N., Strack A., Guan X., Zeng Z., Williams D.L., Feighner S.D., Nunes C.N., Murphy B., Zeng Z., Williams D.L., Jiang Q., Clements M.K., Tan C.P., Mckee K.K., Hreniuk D.L., Mcdonald T.P., Lynch K.R., Evans J.F., Austin C.P., Caskey T., van der Ploeg L.H.T., Liu Q.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor.
SEQUENCE
EMBL; AF242873; AAF82754.1; -. InterPro; IPR00276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1. PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01565; NEUROMEDINUR.
PRINTS; PR01566; NEUROMEDNUIR.
PRINTS; PR01570; NEFFRECEPTOR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                   Caskey T., van der
"Identification of
                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF044601; AAC
EMBL; AF044600; AAC
HSSP; P02699; 1F88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 52:223-229(1998).
EMBL; AF272362; AAG24793.1; -.
EMBL; AF044601; AAC02680.1; -
EMBL; AF044601; AAC02680.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tan C.P., McKee K.K., Liu Q., Palyha O.C., Feighner S.D., Hreniuk D.L., Smith R.G., Howard A.D.;
"Cloning and characterization of a human and murine T-cell orphan G-protein-coupled receptor similar to the growth hormone secretagogue
                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                        NMU1R.
                                                                                                                                                                                                                                                                                                                                                                         Q9JIB2
                                                        Nature
                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000276; GPCR_Rhodpsn
Pfam; PF00001; 7tm_1; 1.
                                                                         eeding."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPFQKHLNSTEEYLAF-LCGPRRSHFFLPVSVVYVPIFVVGVIGNVLVCLVILQHQAMKT
                                                                                                                                                                                                                                                                                                                                                                                                                                              PDSAVCMLVRPRALYNMVVQTTALLFFCLPMAIMSVLYLLIGLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALSVERYVAVVHPLQARSMVTRAHVRRVLGAVWGLAMLCSLPNTSLHGIRQLHVPCRGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTNYYLFSLAVSDLLVLLVGLPLELYEMWHNYPFLLGVGGCYFRTLLFEMVCLASVLNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKTALFETVCFASILSIT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DP--EDINITDEALRIKYLGPQQTELFMPICATYLLIFVVGAVGNGLTCLVILKHKAMRT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity
126; Conserv
                                                        406:70-74(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9782091;
                                                                                     receptors
                                                                                                                                                                                                                                            Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47350 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.9%;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                     for neuromedin U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 680.5; DB 4
Pred. No. 1.5e-55;
2; Mismatches 54
                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F8DD781C020F04AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                         402
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                                                                                   and
                                                                                   its
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Best Local :
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Best Local S
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Q9JJI5;
Q1-OCT-2000
Q1-OCT-2000
Q1-JUN-2002
                                                                                                                                              Receptor.
SEQUENCE
                                                                                                                                                                                                                                                    Fujii R., Hosoya M., Fukusumi S., Kawan Onda H., Nishimura O., Fujino M.; "Identification of neuromedin U as the protein-coupled receptor FM-3."; J. Biol. Chem. 275:21068-21074(2000). EMBL; AB038649; BAA99387.1; -
                                                                                                                                                             PRINTS; PR01237; GPCRRHODOPSN.
PRINTS; PR01565; NEUROMEDINUR.
PRINTS; PR01566; NEUROMEDNUIR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                              InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=20347213; PubMed=10783389;
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1 PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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  75
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                                                           QKAMHTPTNFYLFSLAVSDLLVLLVGLPLELYEMQHNYPFQLGAGGCYFRILLLETVCLA 134
             HQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKTALFETVCFA 129
                                              DSEFKEHFDLEDLNLTHEDLRLKYLGPQQVKQFLPICVTYLLIFVVGTLGNGLTCTVILR 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFHYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKTALFETVCFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVLNVTALSVERYVAVVHPLQAKSVMTRTHVRRMLGAIWVFAILFSLPNTSLHGLSPLYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSEFKEHFDLEDLNLTHEDLRLKYLGPQQVKQFLPICVTYLLIFVVGTLGNGLTCTVILR
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                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                    0 (TremBLrel. 15, 0 (TremBLrel. 15, 2 (TremBLrel. 21,
                                                                                                                                              412 AA;
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                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                   (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                          receptor
                                                                                                                                              46784 MW;
                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Rodentia;
                                                                                                         50.8%;
54.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45782 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.8%;
54.1%;
                                                                                               36;
                                                                                                                                                                                                                                                                                                                                                                                                                           FM-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
                                                                                              Score 642; DB
Pred. No. 5.8e
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 642;
Pred. No. !
                                                                                                                                                                                                                                                                                                                                                                          Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                              2CAB56299E2EA7B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB576083D9F7A095 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                               Kawamata Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412
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                                                                                                                                                                                                                                                                                        cognate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
5.7e-52;
                                                                                                                      DB 11;
                                                                                                          .8e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ĀΑ
                                                                                                                                                                                                                                                                                                                                                                          Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                              64;
                                                                                                                                                                                                                                                                                                               Habata
                                                                                                                                                                                                                                                                                        ligand
                                                                                                                      Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                           Murinae;
                                                                                                                                                                                                                                                                                                               Υ.,
                                                                                                                                                                                                                                                                                        of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402;
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                                                                                                                                                                                                                                                                                                               Hinuma
                                                                                              6
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130

SILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFHYF 189

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OX NEE PER CONTRACTOR
                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 118; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                 Q9VFN4;
01-MAY-2000
01-MAY-2000
01-JUN-2002
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0237; GPCRRHODOPSN.
PRINTS; PR01565; NEUROMEDINUR.
PRINTS; PR01566; NEUROMEDNUIR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

McKee K.K., Tan C.T., Liu J., Palyha O.C., Feighner S.D.,

Hrenluk D.L., Smith R.G., Howard A.D.;

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF044602; AAC02681.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Orphan G protein-couple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  055040
                                                                                                 CG9918
                                                                                                                 CG9918
                                                                                                                                                                                                             Q9VFN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00001; 7tm_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1341898; Gpr66.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 055040;
                                                                                                                                                                                                                                                                                                                                                                                                                       128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190
                                                                                                                                                                                                                                                                                                         183
                                                                                                                                                                                                                                                                                                                           188 YFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRV 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 LQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKTALFETVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 WPYQP--ED-----LNLTDEALRLKYLGPQQMKQFVPICVTYLLIFVVGTLGNGLTCTVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 WIYQQKLEDPFQKHLNSTEEYLAF-LCGPRRSHFFLPVSVVYVPIFVVGVIGNVLVCLVI
                                                                                                                                                                                                                                                                                                     TVPCRGPVPDSAICSLVGPMDFYKLVVLTTALLFFCLPMVTISVLYLLIGLRL
                                                                                                                                                                                                                                                                                                                                                                              FASILSITTVSVERYVAILHPERAKLQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRNKTMRTPTNFYLFSLAVSDMLVLLVGLPLELYEMQQNYPFQLGASACYFRILLLETVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRV
                                                                                                               protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein-coupled receptor.
                                                                                                                                 ) (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      405 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45609 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.28;
50.68;
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06, Last sequence up
21, Last annotation
                                                                                                                                 13,
13,
21,
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                                                                                                                                 Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 596;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomı;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F1BA493D3EB81F34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                           428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11;
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                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                      Insecta;
                                       Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Baradon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Barley R.M., Bassan A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Abril J.F., Agbayani A., An H. J., Andrews-pfannkoch C., Baldwin D.,

RA Ballew R.M., Bassan A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischmann W.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischmann W.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Conference J., Harris M., Glasser K.,

RA Harris N.L., Harvey D., Kelman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Kellen R., Ke Z., Kennison J.A., Ketchum K.A.,

RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Liang Y., Lai Y., Levitsky A.A., Li J., Li Z., Llang Y., Lin X.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshreti A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshreti A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Puri V., Reese M.G.,

RA Nelson D.R., Nelson K., Stapleton M., Strong R., Wenter J., Smith T.,

RA Sylrakas R., Tector C., Turner R., Venter E., Wang S., Yao Q.A.,

                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AE003703; AAF55016.1; -.
ElyBase; FB900038201; CG9918.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00007; GPCRRHODOPSN.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-PROTEIN_RECEP_F1_2; 1.
G-PROTEIN_COUPLED RECEP_F1_2; 1.
G-PROTEIN_COUPLED RECEP_F1_3; 1.
G-PROTEIN_COUPLED RECEP_F1_3; 1.
                 213 IIQVTSFLFYLLPMTVISVLYYLMALRV
                                                        131
                                                                                            153
                                                                                                                                 71
                                                                                                                                                                    93
                                                                                                                                                                                                                                             35
                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                  LLGMPLEVYEMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAK 152
                                                                                                                                                                                                       GPPRDPLAIVIPVTVVYSLIFITGVVGNISTCIVIKKNRSMHTATNYYLFSLAISDFLLL
                                                                                                                                                                                                                                             GPRRS--HFFLPVSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVL
                                                        AMSKLSRAIRIIVLVWIMAIVTAIPQAAQFGIE-HY-
                                                                                            LQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPGSATCTVIKPMWIYNF
                                                                                                                               LSGVPQEVSYIWSKYPYVFGEYICIGRGLLAETSANATVLTITAFTVERYIAICHPFLGQ
                                                                                                                                                                                                                                                                                85; Conservative
                                                                                                                                                                                                                                                                                                    33.1%;
                                                                                                                                                                                                                                                                                    49;
                                                                                                                                                                                                                                                                                                    Score 418;
Pred. No. 4
                                                                                                                                                                                                                                                                                Mismatches
                     240
                                                                                                                                                                                                                                                                                                    .8e-31;
                                                                                                                                                                                                                                                                                                                       DB 5;
                                                        SGVEQCGIVRVIVKHSF
                                                                                                                                                                                                                                                                                                                   Length 428
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                  Gaps
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183 --QLSTFIFFLAPMSIILVLYLLIGVHL 208

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ACCOCC OCCOCC RAPARA RA
          RA Addams N.D., Cclniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams N.D., Cclniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams N.D., Cclniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Galle R.F.,
RA Baltis R.C.,
RA Basta R.F.,
RA Beeson C.R.,
RA Galle R.F.,
RA Galle R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
Q9VFW6
PRINTS: PR00237; GPCRHOODSN.

PRINTS: PR01565; NEUROMEDINUR.

PROSITE: PS00196; COPPER BLUE: UNKNOWN 1.

PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE: PS00237; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; 7

SEQUENCE 595 AA; 65091 MW; 3E8E183BADE
                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: INTEGRAL-!- SIMILARITY: BELONGS TO FAMILY EMBL; AE003699; AAF54929.1; -.
                                                                                                                                                                                                                                          FlyBase; FBgn0038139; CG8795.
InterPro; IPR000923; BlueCu_1.
InterPro; IPR000976; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9VFW6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
a; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13,
13,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                 INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY) FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Last annotation update)
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                                Transmembrane
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RESULT
Q9VFW5
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             Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.

A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

A Jalali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,

A Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

A Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

A Merkulov G., Milshina N.V., Mobarry C., Morris J., McBon D.L.,

Nount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,

A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

A Merkulov G., Nilshina G.S., Pan S., Pollard J., Puri V., Reese M.G.,

A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

A Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

A Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Williams S.M., Woodard M., Weissenbach J.,

Williams S.M., Woodard M., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                     RA Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Annanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Annanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brill J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldvin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayzaktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Danlke C., Davenport L.B., Davies P.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gebatin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Posler C., Gabrielian A.E., Garg N.S., Gebbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Guzandor, I.B. Harris M.,
RA Harris N.I., Harrandor, I. Burnardor, I.B.
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Q9VFW5;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
CG8784 Protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG8784
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13,
21,
Worley K.C.,
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Last annotation updat
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"າດ. 9.
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Wu D.,
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.5e-25;
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RESULT 13
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01-NOV-1996 (Trem
01-JUN-2002 (Trem
C48C5.1 protein.
C48C5.1
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Coulson A.,
Craxton M., Dear S., Du Z., Dubbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                      Q18701
Q18701;
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PRINTS; PRO1565; NEUROMEDINUR.
PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Transmembrane.
SEQUENCE 660 AA; 72277 MW; C52D1EA7E4ACD439 CRC64;
                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                              STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AE003699; AAF54930.1; -.
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000923; BlueCu_1.
InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPFQKH----LNSTEEYLAFLCG------PRRSHFFL--PVSVVYVPIFVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIGVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMALRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPQAMQFSVVYQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLPNTSIHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYY 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLGNLITCIVISRNNFMHTATNFYLENLAVSDLILLVSGIPQELYNLW--YPDMYPFTDA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYP--FLFGPV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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34.1%;
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01,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -NEGYSCIMEND--FYAHVFAVSGFIFFGGPMTAICVLYV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                        Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 337;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                       378
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X., Zhu S., Zhu
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.6e-23;
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Smith H.O.,
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RESULT 14
017239
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                    017239;
017239;
01-JAN-1998
01-JAN-1998
01-JUN-2002
                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Cae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0237; GPCRRHODOPSN.
PRINTS; PRO1565; NEUROMEDIMUR.
PROSITE; PSO0237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
SEQUENCE 378 AA; 43631 MW; 458DC60CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                          STRAIN-BRISTOL N2;
                                                                                                                    Science
                                                                                                                                                                                                          STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                 K10B4.4
                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
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Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Favello A.;
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                                                                  SEQUENCE FROM N.A.
                                                                                                                  investigating biology. The C.
Science 282:2012-2018(1998).
                                                                                                                                     "Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consort
                                                                                                                                                                                       None;
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston R.
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(TrEMBLrel. 05, Las
(TrEMBLrel. 21, Las
1 47.7 kDa protein.
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                                                                                                                                                                                                                                                                                                                       Peloderinae;
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5) to the
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                     Antoniou
                                                                                                                                                                                                                                                                                                                    oda; Chromadorea;
Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last
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EMBL/GenBank/DDBJ databases
  cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 332.5;
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  B.;
K10B4.";
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                                                                                                                                                                                                                                                                                                                                               Rhabditida;
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                                                                                                                                         Consortium.
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RESULT 15
093412
ID 09341
AC 09341
DT 01-N0
DT 01-N0
DT 01-V0
DE Orpha
OS Sphoe
OC Eukar
OC Actir
Retreat
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MEDLINE=20092336; PubMed=10628755;

MEDLINE=20092336; PubMed=10628755;

Palyha O.C., Feighner S.D., Tan C.P., McKee K.K., Hra

Gao Y.D., Schleim K.D., Yang L., Morriello G.J., Narr

A gao Y.D., Schleim K.D., Smith R.G.;

Pilipand activation domain of human orphan growth horn

"Ligand activation domain of human orphan growth horn

"Ligand activation domain of human orphan growth horn

"Ligand activation (GHS-R) conserved from pufferf:

Mol. Endocrinol. 14:160-169(2000).

EMBL: AF082209; AAC33472.1; -

InterPro: IPR000276; GPCR.Rhodpsn.

InterPro: IPR000254; HTH_Gntr.

PFANTS; PR01565; NEUROMEDINUR.

PRINTS; PR01565; NEUROMEDINUR.

PRINTS; PR01565; NEUROMEDINUR.

PRINTS; PR01566; NEUROMEDINUR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                        NCBI_TaxID=39110;
                                                                                                                                                                                                                                                                                                    Sphoeroides nephelus.

Bukaryota; Metazoa; Chordata; Craniata; Verte
Actinopterygii; Neopterygii; Teleostei; Eutel
Acanthomorpha; Acanthopterygii; Percomorpha;
Tetraodontidae; Sphoeroides.
                                                                                                                                                                                                                                                                                                                                                                                 01-NOV 1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
orphan G protein-coupled receptor.
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PRINTS; PR01565; NEUROMEDINUR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Direct Submission.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; AF025463; AAB71009.1; .
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 418 AA; 47735 MW; CE0416539CA3BB27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 IVIMYAHIAVQL 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 VERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTSIHGI--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 YLFSLAVSDLLVILLGMPLEVYE-MWRNYPFLFGPVGCYFKTALFETVCFASILSITTVS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 HLNSTEEYLAFLCGPR--RSHFFLPVSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLFSLAVSDITALILGLPMEFYQSLDYSYPYRFSEGICKARAFLIEFTSYASIMIICCFS 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
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Pred. No. 2.3e-20;
Pred. **hes 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374 AA
                                                                                                                                                                                                                                                                                                                                       Vertebrata; Euteleostomi;
Euteleostei; Neoteleostei
                                                                                                                                               growth hormone (GH)
rom pufferfish to humans.";
                                                                                                                                                                                                                                                                                                                       Tetraodontiformes;
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                                                                                                                                                                                                                 Hreniuk D.L.
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                                                                                                                                                                                                                                                                                              Best Local
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00043; HTH_GNTR_FAMILY; UNKNOWN_1.
                                                                                                      145
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                                                                                                                                                                                                                                                 36 PRRSHEFLP----VSVVYVPIFVVGVIGNVLVCLVILQHQAMKTFTNYYLFSLAVSDLLV 91
                                                                                                 KALVTKRRVRALILLLWTVSLLSAGPVFVMVGVEKDSIMFPNSSDLNESSWPLEAVDTRE
                                             CRMTQYAVESGLMEAMVWL - - - - -
                                                                       CTVIK------PMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRV
                                                                                                                                                          FVC-MPLDLYRMWRYRPWRFGDALCKLFQFVSESCTYSTILCITALSVERYLAICFPLRA 144
                                                                                                                                                                            LLLGMPLEVYEMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRA 151
                                                                                                                                KLQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFH--YFPNGSLVPGSA-----T
                                                                                                                                                                                                                     PPLNYYSIPLLAVITVACTVLFTVGVVGNVMTILVVSRYRDMRTTTNLYLCSMAVSDLFI 85
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                                                                                                                                                                                                                                                                                                                                        374 AA; 42324 MW;
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2003,
                                                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                                                                           Score 303; DB 13; Leng.
Pred. No. 2.3e-20;
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 05:06:39
                                                                                                                                                                                                                                                                                                                                     2CF9304F004C7A16 CRC64;
                                            -SSVFFFMPVFCLTVLYGLIGRRL 246
                                                                                                                                                                                                                                                                                                        Length 374;
                                                                      240
                                                                                                                                                                                                                                                                               34;
                                                                                                                                                                                                                                                                              Gaps
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6,

Search completed: January 17, Job time: 97 secs

Copyright

GenCore version (c) 1993 - 2003

5.1.3 Compugen Ltd

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Database
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Maximum DB
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Gapop 10.0 , Gapext 1.0
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                                                                                     /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AAA46022 AAH49526	AAH43075 AAD01123	AAS98055 AAH43072	AAS98102	AAH50977	AAF85107	ID
Human G protein co Human GTP-binding	Nucleotide sequenc	Human DNA for pote	Human DNA for pote	Human nGPCR15 codi	Nucleotide sequenc	Description

	729 вр.	DNA; 7	standard;	85107	RESULT 1 NAF85107 ID AAF	X D A R
	ALIGNMENTS					
	-					
Genomic sequence o	AAZ4540	99	18.		45	
Human G protein co	21 AAA46116	40	18.		44	
Human GPR38 varian	AA16698	90	18.		43	
cDNA encoding the	21 AAZ45404	90	18.		42	
eotide sequen	8544	9		134.8	41	
	AAF8368	39	18.	134.8	40	
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Short form of moti	AAF8368	61	18.	134.8	38	
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Mouse growth hormo		σ	33.	4	36	
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G-protein cou			64.		22	
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Ф	AAF8032		98.5	717.8	14	
	1 AAZ3	σ	98.5		13	
NMUR2 cDNA	4	4	98.5	7.	12	
G-protein	80		98.5	7	11	
Human G-protein co	24 ABK47909	1248	98.5	717.8	10	

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Nucleotide sequence of human g-protein coupled receptor PFI-002.
                                                               09-JUL-2001 (first entry)
                                                                                                                              AAF85107;
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G-protein coupled receptor; obesity; signal transduction; diabetes; metabolic disease; neurological disease; psychotherapy; dermatology; urogenital disease; inflammation; cancer; tissue repair; photoageing; skin pigmentation; frailty; osteoporosis; cardiovascular disease; gastrointestinal disease; infection; allergy; respiratory disease; sensory organ disorder; sleep disorder; hair loss; gene therapy; PFI-002; ss.

Homo sapiens

CDS 08-OCT-1999; 06-OCT-2000; 11-APR-2001. EP1090990-A1 2000EP-0308852 99GB-0023888 Location/Qualifiers
1..729 /*rag= a /product= "g-protein /*tag= coupled receptor'

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in gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repair, dermatology, skin pigmentation, photoageing, frailty, osteoporosis, cardiovascular disease, gastrointestinal disease, infection, allergy and respiratory disease, sensory organ disorders, sleep disorders and hair loss. The polynucleotide may also by useful
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treating disea
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                     TTCTTCCTCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGTCATTGGCAAT
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ATCCATGGCATCAAGTTCCACTACTTCCCCAATGGGTCCCTGGTCCCAGGTTCGGCCACC
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DB; AAB68333.
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PFIZER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 42; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence encodes a human G-protein coupled
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P-PSDB;
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                                                               New G protein-coupled polynucleotide useful
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                                                                                                                                                                                                                            Vogeli
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V, Sejlitz T, Hu
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Claim

Page

78-79;

261pp; English

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CC The present invention relates to novel G protein-coupled receptors CC (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, CC 28, 31-38, 40, 41, 53-60) and their coding sequences. The present CC sequence is the coding sequence for one such G protein-coupled receptor. CC GPCRs are also known as seven transmembrane receptors and function in CC signal transduction. The nGPCRx coding sequences are useful for CC screening a human to diagnose a disorder affecting the brain or a genetic cerening a human to diagnose a disorder affecting the brain or a genetic confect in a sample is useful for treating schizophrenia. Detection of CC nGPCRx in a sample is useful for treating schizophrenia. Detection of CC disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CC GNS disorders, infections such as HIV-1, metabolic and cardiovascular CC diseases, proliferative disorders and hormonal disorders. Modulators of CC nGPCRx activity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-hyperactivity diseases, Parkinson's disease, migraine and senile dementia. Altheimer's disease, Parkinson's disease, migraine and senile dementia. CC disease), rheumatoid arthritis, autoimmune disorders, cancers, crespiratory ailments such as asthma, and inflammatory diseases e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 729;
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Pred. No. 4.1e-148;
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ID AAS98102 standard; DNA; 813 BP
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DT 12-MAR-2002 (first entry)
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Human; G protein-coupled recep
KW Human; G protein-si; basal cell ca
chordrosarcoma; chronic obstru
KW depression; epilepsy; macular
KW depression; epilepsy; macular
KW depression; epilepsy; macular
KW depression; epilepsy; macular
KW psoriasis; rheumatoid arthriti
KW tuberculosis; cognition disorder; car
KW pain perception disorder; car
KW diabetes; hyperlipidaemia; str
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DA Homo sapiens.
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S Homo sapiens.
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11-MAY-2001; 2001WO-US15332.
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                                  The invention relates to an isolated polypeptide encoded by a nucleic acid molecule that is at least 80% identical to the G protein-coupled (GPCR) polynucleotides included in the specification. Also included are probes based on the GPCR sequences (including antisense probes), a host cell comprising an expression vector comprising the GPCR sequence, antibodies raised against the polypeptides. The golypeptides are useful for identifying modulators of the polypeptides. The polypeptides are useful for identifying modulator compounds which function as modulators, activators, repressors, agonists or antagonists of the novel GPCR polypeptides including the GAL4 polypeptide. The antibodies and nucleic acid probes as described above can be used to detect the presence of the polypeptides and nucleic acids and are used to diagnose a variety of diseases or disorders in which GPCRs are involved e.g., Alzheimer's disease, amyottophic lateral sclerosis, asthma, atherosclerosis, basal cell carcinoma, breast carcinoma, cardiomyopathy, chondrosarcoma, chronic obstructive pulmonary disease, Crohn's disease, depression, epilepsy, macular degeneration, lymphoma, melanoma, cardiomyopathy, of arthritis, osteoporosis, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis; cognition disorder; memory disorder; anorexia; hormonal release disorder; cardiovascular activity disorder; pain perception disorder; obesity; diabetes; obesity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel G protein-coupled receptor polypeptides including galanin receptor polypeptides useful for identifying modulators that are useful for treating Alzheimer's disease, psoriasis, melanoma, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Page 79; 144pp; English.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tuberculosis and many other diseases listed in the specification. The probes and antibodies are also useful for diagnosing cognition and memory disorders, anorexia, hormonal release disorders, cardiovascular activity disorders, pain perception disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds that decrease or increase the expression of galanin receptor (GAL4) caused to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR nucleic acid is useful for treating the above mentioned disorders by gene therapy techniques. The present sequence is a novel GPCR polynucleotide of the
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Pred. No. 4.1e-148;
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depression; epilepsy; macular degeneration; lymphoma; melanoma; multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disea; psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis; tuberculosis; cognition disorder; memory disorder; anorexia; hormonal release disorder; cardiovascular activity disorder; pain perception disorder; obesity; diabetes; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor; Alzheimer's disease; amyotrophic lateral sclerosis; asthma; atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy; chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease;
                                                                 Novel G protein-coupled receptor polypeptides including galanin receptor polypeptides useful for identifying modulators that are useful for treating Alzheimer's disease, psoriasis, melanoma, multiple sclerosis, stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAY-2000;
18-MAY-2000;
Disclosure; Page 120-121; 144pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetes; hyperlipidaemia; stroke; gene therapy
                                                                                                                                                                                                                                                                                                                                                                       (LIFE-) LIFESPAN BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-2002
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                                                                                                                                                                                                                                                                                                     Miller M,
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2000US-205945P
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                                                                                                                                                                                                                                                                                                     Fabre-Suver
                                                                                                                                                                                                                                                                                                     C,
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The invention relates to an isolated polypeptide encoded by a CC nucleic acid molecule that is at least 80% identical to the G protein-coupled (GPCR) polynucleotides included in the specification. CC Also included are probes based on the GPCR sequences (including cthe GPCR sequence), a host cell comprising an expression vector comprising cthe GPCR sequence, antibodies raised against the polypeptides. The GPCR sequence of identifying modulators of the polypeptides. The cc and methods of identifying modulators of the polypeptides. The CC function as modulators, activators, repressors, agonists or antagonists of the novel GPCR polypeptides including the GAL4 polypeptide. The CC antibodies and nucleic acid probes as described above can be used to detect the presence of the polypeptides and nucleic acids and are used to CC diagnose a variety of diseases or disorders in which GPCRs are involved ce.g., Alzheimer's disease, amyotrophic lateral sclerosis, asthma, atherosclerosis, basal cell carcinoma, breast carcinoma, cardiomyopathy, CC chondrosarcoma, chronic obstructive pulmonary disease, Crohn's disease, amyotropic selections, pepilepsy, macular degeneration, lymphoma, melanoma, collitic contributes in the collitic sclitics of the collitic sclitics of the collitics and are the collitics. psoriasis, rheumatoid arthritis, schizophrenia, ulcerative colitis, tuberculosis and many other diseases listed in the specification. The probes and antibodies are also useful for diagnosing cognition and memory disorders, anorexia, hormonal release disorders, cardiovascular activity disorders, pain perception disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds that decrease or increase the expression of galanin receptor (GALA) can be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR nucleic acid is useful for treating the above mentioned disorders by gene therapy. techniques. present sequence is above mentioned disorders by gene therapy a novel GPCR polynucleotide comprising 5

RESULT 4
AAS98055
ID AAS9

AAS98055 standard;

DNA;

1239

SS

Sequence

1239

BP;

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AAH43072
ID AAH4
XX AAH4
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                                                         hypertension;
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24-FEB-2000;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a human TGR-1 protein. The specification describes a method of screening a compound, which is capable of binding properties of neuromedin U to TGR-1. The method is useful for screening preventatives and remedies for hypertension, stress diseases, etc.. TGR-1 antagonists are also useful for treating the same diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying predicted or actual structures of two chemical or physical library by mass spectrometry correlating molecular mass measurements of two or shared chemical history .
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                                                                                                                                                                                                                                                                                                                           Sequence 1245 BP;
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CGCTACGTGGCCATCCTACACCCGTTCCGCGCCCAAACTGCAGAGCACCCGGCGCCGGGCC
                                                                                             CTCTTCAGCCTGGCGTCTCTGACCTCCTGGTCCTGCTCCTTGGAATGCCCCTGGAGGTC
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DB; AAG63353.
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Pred. No. 1.2
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The present sequence encodes a human TGR-1 protein. The specification describes a method of screening a compound, which is capable of bindi properties of neuromedin U to TGR-1. The method is useful for screeni
                                                                                                                                                Identifying predicted or actual structures of two chemical or physical library by mass spectrometry correlating molecular mass measurements of two or shared chemical history -
                                                                                                                                                                                                                                                                                             WPI;
                                                                                                Disclosure; Page 85-87; 95pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000; 2000JP-0032773.
24-FEB-2000; 2000JP-0052252.
30-MAR-2000; 2000JP-0097896.
19-JUN-2000; 2000JP-0187536.
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DB; AAG63366.
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for screening

Human; orphan G Human orphan G

protein-coupled receptor; GPCR; hRUP6; drug

screening;

protein-coupled

receptor hRUP6 cDNA

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The present sequence is a cDNA encoding hRUP6, an endogenous human corphan G protein-coupled receptor (GPCR). The full length hRUP6 cDNA was cloned by RT-PCR using human thymus cDNA as template.

The orphan GPCR of the invention, like all GPCRs has seven transmembrane alpha helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR agonists and antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue localisation expression analysis to provide information about their function in healthy and pathological states.
                                    Query Match
Best Local Similarity
Matches 719; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 - MAY 1999
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16-FEB-1999;
26-FEB-1999;
12-MAR-1999;
12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 21; Page 56-57; 102pp; English.
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receptor;

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Matches
                                                                                                                                                                                                                                                                                                  The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAY-1999;
30-JUN-1999;
27-AUG-1999;
03-SEP-1999;
29-SEP-1999;
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28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
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12-MAR-1999;
12-MAR-1999;
12-MAR-1999;
12-MAR-1999;
12-MAR-1999;
12-MAR-1999;
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12-NOV-1998;
20-NOV-1998;
27-NOV-1998;
16-FEB-1999;
                                                                                                                                                                                                                                                                     Sequence 1248 BP;
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CTCTTCAGCCTGGCGTCTCTGACCTCCTGGTCCTGCTCCTTGGAATGCCCCCTGGAGGTC
                                    GTCCTGGTGTGCCTGGTGATTCTGCAGCACCAGGCTATGAAGACGCCCACCAACTACTAC
                                                                                    TTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGGTCATTGGCAAT
                                                                                                                                   AAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGGACCTCGGCGCAGCCAC
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                       GTCCTGGTGTGCCTGGTGATTCTGCAGCACCAGGCTATGAAGACGCCCCACCAACTACTAC
                                                                                                                                                                       ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG
                                                                       TTCTTCCTCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGGTCATTGGCAAT
                                                                                                                      AAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGGACCTCGGCGCAGCCAC
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719; Conserv
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iaw CW, Lin I,
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990S-0123945.
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990S-0123949.
990S-013637.
990S-0136439.
990S-0136439.
990S-0137131.
990S-0137131.
990S-0141448.
990S-0156553.
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tz K, White
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31-MAR-2000;
23-MAY-2000;
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                                                          Sugiyama
                                                                    Matsumoto
                                                                                                                                                        05-JUL-2001.
                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                          guanosine triphosphate;
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DB; AAG64297.
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2000JP-0101339.
2000JP-0155978.
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Family of guanosine t genes encoding them : with these receptors

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atches 719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the coding sequence for a human guanosine triphosphate (GTP)-binding protein-coupled receptor. The receptor is useful for the investigation, diagnosis, treatment and prevention of diseases associated with GTP-binding protein-coupled receptors, including neurological, circulatory, digestive system, immune system, muscle and urinary system disorders. GTP-binding proteins are also known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1248 BP;
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99.7%;
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RESULT 10 ABK47909 ID ABK47

ABK47909 standard; cDNA; 1248

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В QУ

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ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG

69 60

TTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTTTGTGGTGGGGGGTCATTGGCAAT

Matches Query Match

719;

Conservative

0;

Mismatches

1.2e-145; nes 2; DB 24;

Indels

0;

Gaps

0

Length 1248;

Local Similarity

98.5%; 99.7%;

Score 717.8; Pred. No. 1.

Sequence 1248 BP;

269

A; 392 C; 269 G; 318 T; 0 other;

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The invention relates to a human G protein-coupled receptor AXOR34 and the polynucleotide encoding it. The sequences of the invention are used for treating and/or a variety of diseases, including bacterial, fungal, protozoan and viral infections (particularly infections caused by HTV), pain, cancers, diabetes, obesity, anorexia, bulimia, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders (including anxiety, schizophrenia, manic depression, depression, delirium, dementia and severe mental retardation) and dyskinesias (such as Huntington's disease and Gilles de la Tourette's syndrome). This sequence represents cDNA encoding the human AXOR34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fungal infection; protozoan infection; viral infection; hypertension; parkin; diabetes; obesity; anorexia; bulimia; Parkinson's disease; stroke; acute heart failure; hypotension; urinary retention; osteoporosis; ulcer; angina pectoris; myocardial infarction; benign prostatic hypertrophy; allergy; migraine; vomiting; psychotic disorder; neurological disorder;
                                                                                                                                                                                                                                                            Claim
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P-PSDB; AAU77155.
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                                                                                                                                                                                                                                                                                        treatment of e.g. infections and cancer
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/product= "Human AXOR34"
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BEECHAM PLC.
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                                                                                                                 dermatological; psoriasis; Parkinson's disease; nausea; bulimia; allergy Alzheimer's disease; AIDS; hormonal disorder; memory disorder; migraine; cardiovascular disorder; renal disorder; bone disease; delirium; asthma; Cushing's disease; dysmenorrhoea; antianginal; cytostatic; osteoporosis; metabolic disorder; behavioural disorder; Addison's disease; dyskinesia;
                                                                                                                                                                                         respiratory disorder; depression; schizophrenia; dementia; obesity; pain; gastrointestinal disorder; hypertension; hypotension; epilepsy; diabetes; ischaemia; stroke; cancer; sexual disorder; circadian disorder; anorexia;
                                                                                                                                                                                                                                      Human; G-protein coupled receptor; SNORF72; neuromedin U neuropeptide; NMU; inflammation; arthritis; autoimmune disease; septicaemia; psychotic; mental retardation; transplant rejection; neurological disorder; anxiety;
                                                                                                                                                                                                                                                                                                  Human G-protein coupled receptor, SNORF72 cDNA.
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                                                                                                      antiulcer;
                               Location/Qualifiers 27..1274
              /*tag=
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"Human SNORF72 receptor"
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GTCCTGGTGTGCCTGGTGATTCTGCAGCACCAGGCTATGAAGACGCCCCACCAACTACTAC

240 215

TTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGGTCATTGGCAAT 180

TTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGTCATTGGCAAT

AAACACCTGAACAGCACCGAGGAGTATCTGGGCCTTCCTCTGCGGAGCCTCGGGCGCAGCCAC 120 ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG

AAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGGACCTCGGCGCAGCCAC

155

Matches

Conservative

0,

Mismatches

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Indels Length

0;

Gaps

0;

95 60 Query Match Best Local Similarity

98.5%; 99.7%;

Score 717.8; DB 22; Pred. No. 1.2e-145;

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CC The invention relates to human G-protein coupled receptors, SNORF62 and CSNORF72 and their corresponding cDNA molecules. SNORF62 and sNORF72 CC receptors are specific for neuromedin U (NMU) neuropeptides, hence they CC are also known as NMU receptors. The agonist and antagonist of NMU corresponding to treating an abnormality in a subject that is alleviated by decreasing or increasing the activity of NMU receptor. CC The NMU receptors serves as a valuable tool for designing drugs which are useful for treating various pathophysiological conditions such as inflammation, arthritis, autoimmune diseases, transplant rejection, CC graft vs host disease, bacterial, fungal, protozoan and viral infections, cc septicaemia, AIDS, pain, psychotic and neurological disorders, including can anxiety, depression, schizophrenia, dementia, mental retardation, memory cc loss, epilepsy, neuromotor disorders, respiratory disorders, asthma, CC eating/body weight disorders including obesity, bulimia, diabetes, anorexia, nausea, hypertension, hypotension, vascular and cardiovascular cd disorders, renal disorders, bone diseases including osteoporosis, benign cc disorders, prenal disorders, such as psoriasis, allergies, Parkinson's cd disease, Alzheimer's disease, acute heart failure, angina disorders, delictium and dyskinesias such as psoriasis, epinephrine release cd disorders, electrolyte balance disorders, epinephrine release cd disorders, electrolyte balance disorders, endocrine disorders, memory alsorders metabalic disorders memory alsorders memory alsorders memory alsorders metabalic disorders memory.
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                                                                                        disorders, somatosensory disorders, metabolic disorders, behavioural disorders, drug addiction, migraine, Addison's disease, Cushing's disease, prevent miscarriage, induce labour or to treat dysmenorrhoea
  Sequence
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30-JUN-2000;
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                                                                     The present cDNA sequence encodes human G-protein coupled receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a purified mammalian SNORF62 or SNORF72 receptor protein for identification of compounds to treat e.g. inflammation, arthritis,
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BP; 278 A; 405 C; 282 G; 333 T; 0 other;
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                                                                                                                                                                                                Human NMUR2
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Ploeg
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Query Match
Best Local S
Matches 719
                                                                                                                                            The invention relates to human and rat neuromedin U receptor designated NMUR2 polypeptides and polypuclectides. NMUR2 also referred as FM-4, is free from associated proteins and is involved in the feeding behaviour in mammals. Sequences of the invention are useful for identifying compounds which modulate the feeding activity of a mammal. The compounds identified are useful for modulating eating and weight gain. The present
                                                                                                                                                                                                                                                                                                                                     New polypeptide, useful for identifying compounds feeding activity of a mammal, comprises the novel rat neuromedin U receptor designated NMUR2 -
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                                                                                                                                                                                                                                                                                                  Example 1;
                                                                                      Sequence 1344 BP;
                          Similarity
                                                                                                                             is human
                                                                                                                                                                                                                                                                                              Fig
        Conservative
                                                                                      291 A; 419 C; 290 G;
                                                                                                                                                                                                                                                                                                47pp;
                                                                                                                               NMUR2 cDNA.
                          98.5%;
                                                                                                                                                                                                                                                                                                English.
      0;
      Score 717.8; DB Pred. No. 1.2e-1:0; Mismatches
                                                                                      344 T; 0 other;
; DB 24;
1.2e-145;
2;
                                                                                                                                                                                                                                                                                                                                                               which modulate isolated human
        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG
                                                                                                                      TTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGTCATTGGCAAT
                                                                                                                                                                                                   GCCCTCTTTGAGACCGTGTGCTTCGCCCTCCATCCTCAGCATCACCACCGTCAGCGTGGAG
                                                                                                                                                                                                                                    TATGAGATGTGGCGCAACTACCCTTTCTTGTTCGGGCCCGTGGGCTGCTACTTCAAGACG
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                                                  TATGAGATGTGGCGCAACTACCCTTTCTTGTTCGGGCCCGTGGGCTGCTACTTCAAGACG
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                                                                                                                                                                                                                                                                        CTCTTCAGCCTGGCGGTCTCTGACCTCCTGGTCCTCCTTGGAATGCCCCTTGGAGGTC
                                                                                                                                                                                                                                                                                                                                                                                      ANACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGGACCTCGGCGCAGCCAC
                 TTCTACCTCCCCCATGACTGTCATCAGTGTCCTCTACTACCTCATGGCACTCAGACTA
                           TTCTACCTCCTCCCCATGACTGTCATCAGTGTCCTCTACTACCTCATGGCACTCAGAGTG
                                                                                                                                                                                            GCCCTCTTTGAGACCGTGTGCTTCGCCTCCATCCTCAGCATCACCACCGTCAGCGTGGAG
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AAZ33297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Sim
Matches 719;
                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a human G-protein coupled receptor neurotensin-like receptor (NIR). The NLR polynucleotide and protein can be used to isolate compounds that bind, (ant)agonise or alter the activity or expression of the NLR. The NLR is a G-protein coupled receptor which is expressed in the central nervous system and shares homology with human neurotensin receptor. The receptors can be used in
                                                                                                                                                                                                                                                                                                                              Sequence 1360 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel neurotensin-like receptor, useful for identifying agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ahmad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09955732-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; neurotensin-like receptor; NLR: G-protein coupled receptor; central nervous system; anasthesia; analgesia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ33297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ33297 standard;
 301
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                                                                                                                                                                            134
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                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                         ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG
                                     CTCTTCAGCCTGGCGGTCTCTGACCTCCTGGTCCTGCTCCTTGGAATGCCCCCTGGAGGTC
                                                                         TTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGTCATTGGCAAT 180
                                                                                                                                                                                      AAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGGACCTCGGCGCAGCCACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
TATGAGATGTGGCGCAACTACCCTTTCTTGTTCGGGCCCGTGGGCTGCTACTTCAAGACG
                        CTCTTCAGCCTGGCCGTCTCTGACCTCCTGGTCCTTGGAATGCCCCTGGAGGTC
                                                                                               GTCCTGGTGTGCTGGTGATTCTGCAGCACCAGGCTATGAAGACGCCCCACCAACTACTAC
                                                                                                                        TTCTTCCTCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGTCATTGGCAAT
                                                                                                                                                                          AAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGGACCTCGGCGCAGCCAC
                                                                                                                                                                                                                          ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-052803/04.
)B; AAY52992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurotensin-like
                                                                                                                                                                                                                                                                                                                                                       ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASTRA AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 1; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anasthesia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cao J,
                                                                                                                                                                                                                                                                                                                                                   identify agents for producing anasthesia and analgesia
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHARMA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98SE-0001455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-SE00598
                                                                                                                                                                                                                                                                                                                            293 A; 423 C; 294 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0'Donnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry]
                                                                                                                                                                                                                                                                                         98.5%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analgesia
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                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                            Pred. No. 1.2e-145;
D; Mismatches 2;
                                                                                                                                                                                                                                                                                                   Score 717.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Walker
                                                                                                                                                                                                                                                                                                                          350 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ψ,
                                                                                                                                                                                                                                                                                                    DB 21;
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                                                                                                             24-SEP-1999;
24-SEP-1999;
28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; G-protein coupled receptor; IGS4; IGS4A; IGS4B; schizophrenia; nervous system disorder; psychiatric disorder; Parkinson's disease; episodic paroxysmal anxiety; phobia; migraine; epilepsy; bulimia; stroke; cardiovascular disease; heart failure; angina pectoris; obesity; emesis; motility disorder; myocardial infarction; hypertension; dyslipidemia; motility disorder; myocardial infarction; hypertension; dyslipidemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gynecological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gastrointestinal disorder; inflammatory bowel disease; osteoporosis;
inflammation; infection; pain; cancer; immune disorder; allergy; sep
                                                                                         31-JUL-2000;
                                                                                                                                                                                                              25-SEP-2000;
                                                                                                                                                                                                                                                                                                             WO200125269-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Splice variant of G-protein coupled receptor IGS4A long version cDNA
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                                                                                                                                                                                                                                                              12-APR-2001.
                                          (SOLV)
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                                          SOLVAY PHARM
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99NL-1013140.
2000EP-0202683.
2000US-0222047.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection; pain;
disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
55..945
/*tag= a
                                                                                                                                                                                                                                                                                                                                 DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; immune disorder; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          660
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Deleersnijder

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a splice variant of the long version of a human G-protein coupled receptor designated IGS4A. IGS4 exists in two polymorphic forms, IGS4 and IGS4B. The IGS4 receptors and IGS4 polynucleotides are useful for preventing, ameliorating or correcting dysfunctions or diseases. These diseases include peripheral nervous
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28-JUL-2000;
31-JUL-2000;
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                                                              disorders, or cancers
                                                                      New G-protein coupled receptors and the polynucleotides encoding useful for preventing, ameliorating or correcting nervous system disorders, cardiovascular diseases, dyslipidemias, inflammations,
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The present sequence encodes a splice variant of the short version of human G-protein coupled receptor designated IGS4A. IGS4 exists in two polymorphic forms, IGS4A and IGS4B. The IGS4 receptors and IGS4

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Example 1b; Page 94-95;

102pp;

English.

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hypertension), dyslipidemias, obesity, emesis, gastrointestinal disorders (e.g. inflammatory bowel disease or motility disorders), osteoporosis, inflammations, infections (e.g. bacterial, fungal, protozoan or viral), pain, cancers, immune disorders, altergies, sepsis or gynecological disorders. Agonists or antagonists of IGS4 are effective with regard to disorders of the nervous system, including the central and peripheral nervous systems, disorders of the gastrointestinal system, cardiovascular system, skeletal muscle, thyroid, lung or genitourinary system, or immunological disease. The IGS4 polynucleotides are useful as diagnostic reagents for detecting under-expression,
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overexpression or altered expression of IGS4.
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Sequence 1594 BP; 370 A; 473 C; 332 G; 419 T; 0 other;

Query Match Best Local

Local Similarity

98.5%;

Score 717.8; DB 22 Pred. No. 1.2e-145;

DB 22; Length 1594;

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REFERENCE AUTHORS TITLE JOURNAL

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 729)
Harland, L.P.
Human g-protein-coupled receptor
Patent: EP 1090990-A 1 11-APR-2001;

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/db_xref="taxon:9606"
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1 (bases 1 to 801)

Vogeli,G., Wood,L.S., Parodi,L.A., Hiel

Slightom,J., Schellin,K.A., Kaytes,P.S

Sejlitz,T. and Huff,R.M.

Novel g protein-coupled receptors

Patent: WO 0136473-A 17 25-MAY-2001;

PHARMACIA & UPJOHN COMPANY (US)

Location/Qualifiers
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Kaytes,P.S., Banniga
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Quality: Phrap Quality
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Submitted (03-AUG-1999) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
3 (bases 1 to 214267)
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Finishing Completed at Stanford Human Genome
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DOE Joint Genome Institute and Stanford
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ive, Walnut Creek, CA 94598, USA
Sep 26, 2001 this sequence version replaced gi:15290296
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                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 1239)
Liu,Q., McDonald,T.P.,
Direct Submission
                                                                                                                                                                                                                                                                                                     Submitted (09-MAR-2000) Pharmacology, Point, PA 19486, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
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/translation="MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLP VSVVYVPIFVYGVIGNVLVCLVILQHQMKTPYNYYLFSLAVSDLLVLLLGMPLEVYE MWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVEFXVAILHPFRAKLQSTRTRA LRILGIVWGESYLFSLDHTSHHGIKFHYFPNGSLVPGSATCTVIKPMWIXINFILQVTS FLFYLLPMTVISVLYYLMALRIKKDKSLEADEGNANIQRPCRKSVNKMLFVLVLVFAI
                                                                            /codon_start=1
/product="neuromedin U receptor
/protein_id="AAF82755,1"
/db_xref="GI:9082156"
                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                              /note="FM-4"
                                                                                                                                                             /gene="NMU2R"
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G protein-coupled receptor
Homo sapiens cDNA to mRNA.
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2 (bases 1 to 1248)
Shintani, Y., Moriya, T., Ohkubo, S
Direct Submission
Submitted (03-APR-2000) Yasushi
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Shintani,Y., Fukusumi,S., Habata,Y., Hinuma,S.,
Nishimura,O. and Fujino,M.
Identification and functional characterization
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Hosoya, M., Moriya, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Industries, LTD, Discovery Research Laboratories Tsukuba, Ibaraki 300-4293, Japan (E-mail:Shintani_Yasushi@takeda.co.jp, Tel:81-296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax:81-298-64-5000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="G protein-coupled receptor TGR-1"
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MWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRA
LRILGIYWGFSYLFSLENTSIHGIKFHYEPNGSLVPGSATCTVLKPMWIYNFILQVTS
ELFYLLPMTVISVLYYLMALRLKKDKSLEADEGNANIQRPCRKSVNKMLFVLVLVFAI
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FQNVISSFHKQWHSQHDPQLPPAQRNIFLTECHFVELTEDIGPQFPCQSSMHNSHLPT
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393 c 269 g
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10. .1248
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1. .1248
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99.7%;
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1.2e-125;
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1 (bases 1 to 1298)

Raddatz R., Wilson, A. E., Artymyshyn, R., Bonini, J. A., Borowsky, B., Boteju, L.W., Zhou, S., Kouranova, E. V., Nagorny, R., Guevarra, M.S., Boteju, L.W., Zhou, S., Kouranova, E. V., Nagorny, R., Guevarra, M.S., Boteju, L.W., Zhou, S., Kouranova, E. V., Nagorny, R., Guevarra, M.S., Boteju, L.W., Zhou, S., Kouranova, E. V., Nagorny, R., Guevarra, M.S., Boteju, L.W., Zhou, S., Vaysse, P.J., Branchek, T.A., Gerald, C., Forray, C. and Adham, N.

Identification and characterization of two neuromedin U receptors differentially expressed in peripheral tissues and the central
                                                                                                                                                                                                                                                                                              Bonini,J.A., Raddatz,R., Wilson,A. and Borowsky,B. Direct Submission
Submitted (25-MAY-2000) Target Discovery and Assessment, Pharmaceutical Corporation, 215 College Road, Paramus, N
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J. Biol.
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/product="neuromedin U receptor 2"
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/protein_id="AAG24794_1"
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VZEMMRNYFFLEGPVGCYFKTALFETVCFASILSITTYVSVEKYVAILHPERAKLQSTR
RRALRIGIVAGFSVLESLEMTSIHGIKFHYFPNGSLVPGSATCTVIKMMIYNFIIQ
VTSFLFYLLPMTVISVLYYLMALRLKKDKSLEADEGNANIQRCCRKSNNKMLFVLVLV
FAICWAPFHIDRLFFSFVEEWSESLAAVFNLVHVVSGVFFYLSSAVNPIIYNLLSRRF
                                                                                                                                                                                                                                                                                                                                                                                               Chem.
                                                                                                                                                                 /gene="NMUR2"
27. .127/
                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                         /codon_start=1
                                                                                                                                     /note="G
                                                                                                                                                   /gene="NMUR2"
                                                                                                                                                                                                      /map="5q31.1-q31.3"
                                                                                                                                                                                                                    /chromosome="5"
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LPTALSSEQMSRTNYQSFHFNKT"
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                                                      TGTACGGTCATCAAGCCCATGTGGATCTACAATTTCATCATCCAGGTCACCTCCTTACCTA
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Deleersnijder W., Berger C., Loeken C.,
Human g-protein coupled receptor
Patent: WO 0125269-A 9 12 APR-2001;
Solvay Pharmaceuticals B.V. (NL)
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RRALRILGIVWGFSVLFSLDNTSIHGIKFHYFDNGSLVPGSATCTVIKDMWIYNFIIQ
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/db_xref="taxon:9606"
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Patent: WO 0125269-A II 12-APR-2001;
Solvay Pharmaceuticals B.V. (NL)
Location/Qualifiers
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/db_xref="GI:13924118"
/db_xref="GI:13924118"
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LRILGIVWGFSVLFSLPNTSLHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTS
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                          ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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Patent WO0125269.
                                                       ; Score 717.8;
; Pred. No. 2.2e
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2.2e-125;
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1 (bases 1 to 1658)

Deleersnijder,W., Berger,C., Loeken,C., Nys,G. and Venema,J.
Human g-protein coupled receptor
Patent: WO 0125269-A 12-APR-2001;
Solvay Pharmaceuticals B.V. (NL)
Location/Qualifiers
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64. .1302
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FLFYLLDMTVISVLYVLMALRLKKDKSLEADEGNANIQBPCRSSVNKMLFVLVLVFAI
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Deleersnijder,W., Berger,C., Loeken,C., Nys,G. and V. Human g-protein coupled receptor Patent: WO 0125269-A 5 12-APR-2001; Solvay Pharmaceuticals B.V. (NL)
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FILPVSVYVPIFVVGVLGNVLVCLVILOHQAMKTPTNVYLFSLAVSDLLVLLLGMPLE
VYEMWRNYPLEFGPVGCYFKTALFETVCFASILSITTVSVKYAILHPFRAKLQSTR
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t: WO 0125269-A 7 12-APR-2001;
y Pharmaceuticals B.V. (NL)
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J. Biol. Chem. 275 (50), 39482-39486 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                       Shan, L., Qiao, X., Crona, J.H., Behan, J., Wang, S., Gustafson, E.L., Monsma, F.J. Jr. and Hedrick, J.A. Identification of a novel neuromedin U receptor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1248)
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/translation="MSGMEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHF FLPVSVVYVPIFVVGVIGNULVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLGMPLE VYEMMRNYPFLEGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTR RRALRILGIVMGFSVLFSLPWTSIHGIKFHYFDMGSLVPGSATCTVIKPMMIYMFIIQ VTSFLFYLLPMTVISVLYYLMALRLKKDKSLEADEGNANIQRPCRKSVNKMLFVLVLV
                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                           /product="neuromedin U receptor-type
/protein_id="AAG03064.1"
/db_xref="GI:9944990"
                                                                                                                        /note="G protein coupled receptor; NmU-R2"
/codon_start=1
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IMAGE:3852151,
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Pred. No. 4.5e-125;
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JOURNAL
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ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG
                                      GTCCTGGTGTGCCTGGTGATTCTGCAGCACCAGGCTATGAAGACGCCCACCAACTACTAC
                                                                                                                      TTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGGTCATTGGCAAT
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                                                                                718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.series: IRAK Plate: 20 Row: n Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency OR analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (05-NOV-2001) National Institutes of Submitted (05-NOV-2001) Cancer Genomics Office,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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FAICWAPFHIDRLFFSFVEEWSESLAAVFNLVHVVSGVFFYLSSAVNPIIYNLLSRRF
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VYEMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTR
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/protein_id="AAH16938.1"
/db_xref="GI:16877377"
/translation="MSGMEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Colon, adenocarcinoma"
/clone_lib="NIH_MGC_65"
/lab_host="DH10B"
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/db_xref="Locusin:56923"
/db_xref="taxon:9606"
/clone="MGC:21396 IMAGE:3852151"
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(Dickson, Mark) mcd@paxil.stanford.edu
M., Schmutz, J., Grimwood, J., Rodriquez,
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                                                                                                                                                                                                   Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N. P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavek, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Deuthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flags, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Ganer, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris K.
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Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jackson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.
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AC122979.2 GI:21909359
HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muzny,D.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 165392)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adio-Oduola, B., Ali-osman, F.R.,
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; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Banks,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Allen, C.,
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (26-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 165392)
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Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Dep of Molecular and Human Genetics, Baylor College of Medicine Baylor Plaza, Houston, TX 77030, USA
On Jul 19, 2002 this sequence version replaced gi:21217312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 59 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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Center clone name: CH230-353A10
----- Summary Statistics
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